

1198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

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AGTGCCTTTC CACCTCTTTT TATCTATAAA GATTCTCCTA CATCATAATT CATTFTTTTA	120
TTTAAACCTT TCTGTCTTAG TTTGTCTTTA TCTTCTTCAT ACCATTTTAA GATTGTCACA	180
TAGTGGTTTT GATAGGCTT ACCACTGCTT TCCATGTATC TGGATAGTTT ATTTATCATT	240
ATATCTGTGT GTGAGTTTAA TTTTCTTTT AGATTTTAT ATTCTTCTT GCTTAACCTT	300
ACATTTTGA ATCTCCATA AAAAATGGGG GTGGACTTTT TATCTATCTC TCCCTCTCTC	360
TCTTTATCTA TCTCTATATC TTTCCATGTA ATTCCAATCT GGAGTACCTC TACTGTCTAT	420
CGGTAATTTA ATTTTGATAT CTGGCAATAC TGTGCTAGAT ATTTGATCTT TATATTCAGT	480
ATTTTAAAA GCTTGCCTAA TAATTGAAGT TAAATAGAAT GCTACTTCTT TATTCAATTC	540
TTTATTTTTT AATTTTAAAC AATGAATTTT CATATCTAGG CTTGCTTTAT ATTTATGATA	600
AAAGACTGCT CCTAAAAATC AAACAGATAT AAAATTTTCA AAAACTCTAT AATTTTATC	660
ATCTATATCT TCGTAGTAAC CTAAGATACC ATTGTCAATA TTTGTAGCAC TAATTCTAGG	720
AGTTTTTCCA TCGAGTAAAT ATCTTTTGG AATAGATGAG CCTGTGGTA CTTAACTCGA	780
TTTCCCCTTT TTTTCGGTAA TAAATATTTT TTTTATTTT GTTGTCTGAT ATTTTTCCTA	840
CCTGTCCTTT GTAGGATGAG TATTTCTAG ATTTTCyTGA ATAACTTTTT ACTTGAAGTT	900
TTAGCTTTTG AACTAGTCGT TGTACTTCTT TTTGTTTAT TATCAGTCCT GATCTTTTAA	960
ATATGCTGT TATTCTCTAT ATCCTATTTT TCATTCATGA TATTCTTTTA CTAATTTTAT	1020
CTTAAATCTT GTGCTGTATT TGCCATTAAA AAAGTACCT CTTTAGTTA GTTTTGTGGC	1080
CTAACTTTTG AGGCTCAGTT CAAAATTGCT GACTTTTAAA TGAATTCCAA TATTCAATTA	1140
TTAAGAGTTA ACATGGTGCT TGCCAATAGG AATCATTAGA GGCGAATTGG AAATAGGGTC	1200
ACGTATAATT TTTGCTTCAA GATTAAAGAT ATCTTTAACT AGTTTATCAT TTAGTATATC	1260
TTCAGGCTTT CCCTCTGCAA CAAGTTTACC TTCTTTAATT GCAAATAGGT AATCAGCGTA	1320
TCTTGCTGTT AGATTTATAT CGTGCAAAAT CATGCAAAATG GTTGTCTTAT ATTTTGGTT	1380
TAGATCAGTC AAGAGGTCTA ATAGTTCTAT TTGATATGAG ATATCCAAGT AAGTAGTTGG	1440
CTCATCTAAA AGTAGGATAC TTGTATCTTG GGCTAGGGCT AGAGCTATCC ATACTCTTTG	1500
CCTTTGACCC CCAGAAAGTT CTCAACTAG GTTATTTGCT AGATCTTCAA CATTGGCCTT	1560
AACCATTGAT CTGTTTATTA TTCAAGGTC ATCTTTTCCA AGACTCTTAA AAGGCTTCT	1620
GTAGGGGAAA CGACCACGGC TTACAAGATC AGCTACTGTT ATTGATTCAG GGATTATTGG	1680
AGATTGAGGT AATATAGCTA TGTGTTTGC TAAATCTTTT TCTTTATAAG AATTAATTGA	1740

1199

TTTATTATCA AGCAATACTT CTCCCTCTAA TGGCTTTATA AGTCGAGACA AGGTTTAAAT	1800
GAGTGTGAT TTCCCACAAC CATTGACCC AATAATAACT GATATTTTTT CTTCAGGTAT	1860
TTTATATTT ATATTTTCCA AGATTATTTT TTCATCATAA CCGCAGGTAA GATTATTTGA	1920
CCACAGACCT TTCATTATAT ATTCCTCCTG TTCATTTTTA TTAGTAAGTA TATTAAGTAT	1980
GGTGAACCTA ACAAGCCAGT TACAACACCT ACTGGATATC TAGCTGGTAA AATATTTTGA	2040
GAGAATATGT CTGATAACAA AACTAGTAAA ATTCCAACCA ATCCAGCTAA TATTGGGCTT	2100
CTTTCTTGC CAATATTTAA GGCTATGGGA CCAGCTAAAA AAGATATACA AGCTATTGGT	2160
CCTGTAATTG AAGTAGAAAA AGCAGTTAAA GATACAGCGC AAAAAATTAA AACAAGCCTT	2220
GAAAGCTCGG GATTGCTCC AAGTCCGATT GCTATTCTT CACCAAGTTC AATAATTTCT	2280
AGTCTTTTAT TAAAAAATAA AACTAATATA GTAGCAATAA TACTTACTAT TAGAACAAGA	2340
GGTATGTCAT CTAACCTTGT AAAAGATAAA GAGCCACTGA GCCATCTCAT AACTTCTTGT	2400
AATTCATATC TTGCTACTTT CAACAATAAA AATGAGGTGC CTGCTCTTGT GACAGCTTGA	2460
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AATAATATTA AAGATGATGT TAGTCCACAA GTTATTGAAA TAATFCCAGT AGTTAAACTA	2580
TTTGTTTTAA ATACCAATAT GCAAAAGACC GCTGCAATAG ATGAAGAACT TGTGACACCG	2640
ATTATATCAG GACTTGCAAG AGGATTCTTT AACATAGTTT GAAAGATAAA TCCTGCCAAT	2700
CCAAAAGACC AGCCAGCTAT AATCCTGCT AATAATTTTG GTAATCTAAT TTCCATAATC	2760
GAAAACTAG CTCCAGGAAC AGTTTCACTA TTAAAGACTT TAATCAAAGT TGAAAAAGAA	2820
TAACCTTCAT CTCCGATAAG TAAAAAGAAA AATGATAGAC TGATTATTAT TAATAAAAAAT	2880
AGTGAGGAAA ATAGTGTTAT TCTATTTTTT CTTTTTGA TACCTATAAT TAAATTTTGC	2940
ATTAGTTATT AACCCCTCTA TTTTTCATAG TTACATAAAAT AAGTACTGGA CCCCCGATTA	3000
TTGCAGTAAT TATCCCTACT TCAATTTCAC CTGGTTTACC TAACATACGG CCGATTATAT	3060
CACATATAAG CAAGAGCTCT GCACCTATAA AAGATGAAGA AATGGTCATT GTGCGTATAT	3120
CTTTGCTTAT AAATAAGCCA CAAAAGTGAG GAACTATAAG ACCTACGAAG CCAATAGGTC	3180
CACCAATTGC AGTAATACTT GAACATAAAA GCACACTTGC AATTATTGCA AGTGATCTTA	3240
TCCTATTAAC ATTAACCTCA AGACCAACAG CCATTTCATC ACCCATAGCT AAAGCGTTTA	3300
AATCTGATGA AATAAATATA GCTATCAAGT GACCTAAAAT TATAAAAGGT AGTAGTGTAG	3360
ATATAGAAGA TAATGTAGCT GCTCCAAGGC TACCTATTTG CCAAAATCTA AATTTGTCTA	3420
AGACGTTATT ATTCGGTAAA ATTAAAAAAC TTACAAAACT GCTTAAAGCC ATACTAACAC	3480

1200

AAGTTCCTGA TAAGGCAAGT TTTATAGGGG TAAGGCCTGC TTTTCCGTTA CAGCAATCGC	3540
GTATACAAAA ATTGCACTTA CTAAGCCACC AATGATTGCG	3580

## (2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11378 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

CCAAATTGCT CCACAATTAT TATGGAGTCG TCGTTTGGCA GATGGCCGTG ATATCTGTGC	60
TCAAGAATGG TTGACAGGCA AGATATTGAC CCCCTATGAT ATGAATCGTA AGCAAATCGT	120
CAATATTTTA ACCCGTCTTC ATCGCTCACG TCCGTTGATG ACACAATTGA GTCGTTTGGG	180
CTATGCCATG GAAACACCTG TAGATTACT ACAGTCTTGG CAGGAAACGG CTCCAGATGC	240
TTTGCGTAAA AATCATTTTA TCAGTGAAGT GATGGCTGAT TTACGTCAGA CTATTCCAGG	300
ATTTAGAGAG GACCATGCCA CCATTGTCCA TGGAGATGTA CGACATAGTA ATTGGATTGA	360
GACAGATAGT GGCTTGATTT ATTTAGTAGA TTGGGATTCG GTTCGCTTGA CCGATCGCAT	420
GTTTGATGTG GCCCATATGC TCTGCCATTA TATTTAGAA CATCAGTGGA AGGAATGGTT	480
GACCTACTAC GGTTACAAGT ACAATCAAAC GGTATTAAGT AAATGTATT GGTATGGTCA	540
ATTGTCTTAT TTGAGTCAGA TTTCCAAGTA TTATATGAAC CAAGATTTAG AAAATGTCAA	600
TCGGGAGATT CATGGTTTGC GTCAATTCCG AGACAAGTAT GGAAGAGAA GATGAGAGTT	660
AGAAATCGTA AAGGGGCAAC AGAATTACTA GAGGCAAATC CCCAGTATGT GGTCTCTAAT	720
CCCTTGGAAG CCAAGGCAAA ATGGCGGGAC TTGTTTGGCA ATGATAATCC CATTCATGTG	780
GAAGTTGGAA GTGGAAGGG TGCCTTTGTT TCAGGTATGG CCAAGCAAAA CCCTGACATC	840
AACTATATCG GGATTGATAT TCAAAAGTCT GTTTTGAGCT ACGCTTTGGA CAAGGTGCTT	900
GAAGTTGGAG TGCCTAACAT CAAGCTCTTG TGGGTAGATG GTTCTGACTT AACTGACTAC	960
TTTGAAGACG GTGAGATTGA TCGCTTGAT CTGAACTTT CAGATCCATG GCCGAAAAAA	1020
CGCCATGAAA AGCGTCGTTT GACCTACAAG ACCTTCTTGG ATACCTTCAA ACGTATCTTG	1080
CCTGAAAATG GAGAAATTCA TTTCAAGACG GATAACCGTG GCTTGTTTGA GTACAGTTTA	1140
GTGAGCTTTT CTCAATATGG CATGAAATC AATGGTGTCT GGTAGATTT GCATGCCAGT	1200
GATTTTGAAG GCAATGTCAT GACAGAATAC GAGCAAAAAT TCTCAAACAA GCGGCAAGTT	1260
ATCTACCGAG TTGAGGCAGA ATTTTAAGAG ATAACCTAAA ATTAGGCTGT ACAAGTGCTT	1320

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TTGCTTTACA TAAGTTGGCA AACGTGCTAT ACTGATAGTA AGAATATGAA AAGTGAGGCG	1380
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TAGTCAGAGA AGTTGTAGAA CCTGTCATAG AAGCTCCTTT TGAACTCGTG GATATCGAGT	1500
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CTTGAACGAC ACGGCAGACT TGACAGAAAT TATCAGTCCT GTCCTAGACA CCATCAAGCC	1620
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AGCCATCGAT AAGCAAAAGG TCTTTGAAGG AACCTTGTTG GCCTTCGAAG AGGACGAGTT	1800
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AAGAAGCACC AGCTGAGTTT GGTGCTGTAG CAGCCCAATC TGCCAAACAA ACCATCATGG	2280
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GACAAAACGT GCGCTTGGCG GCTCACTTGA CTGGTTACCG TATCGATATC AAGTCTGCTA	3000
GCGAATTTGA AGCCATGGAA GACGCTGCTT CAGTAGAGTT GGAAGTAGAA AACGATACTG	3060

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AGTCTGTGTGT GTCTAACGAA GTGATTGATA AGCGTGATTT GCTCCGCAT TGTCAAGAACA	3180
AGGAAGGACA AGTCTTTATT GATcCTACGG GCAAGGCCAA TGGCCGCGGC GCTTATATCA	3240
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AAAGAAGAGA GTTGGGACTT GAATAAGCAA AAGATAAGTA ATCTCTTGGG GCTTGCTCAG	3420
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CAAAAAGGC AATAACAAGA ACAACCGTAA TCAGACTCCA AAACCTGTTA CGGAGCGTAA	4800
ATTCCATGAA TTGCCAACAG AATTTGAATA TACAGATGCT ATGACCGTTG CGGAAATCGC	4860

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TATCGAAGCC AAACAAAAGG TTGAAGTGA TAATGCTGAC ATCGAACGTT TCTTTGTCGA	5040
AGATGGTTAT CTCAATGAAG ATGAATTGGT TGAGCGTCCA CCAGTTGTTA CTATCATGGG	5100
ACACGTTGAC CACGGTAAAA CAACCCCTTT GGATACTCTT CGTAACTCAC GTGTTGCGAC	5160
AGGTGAAGCA GGTGGTATTA CTCAGCATAT CCGTGCCTAC CAAATCGTGG AAAATGGTAA	5220
GAAGATTACC TTCCTTGATA CACCAGGACA CGCGGCCTT ACATCAATGC GTGCGCGTGG	5280
TGCTTCTGTT ACCGATATTA CGATCTTGGT CGTAGCGGCA GATGACGGG TTATGCCTCA	5340
GACTATTGAA GCCATCAACC ACTCAAAAGC AGCTAACGTT CCAATCATCG TAGCTATTAA	5400
CAAGATTGAT AAACCAGGTG CTAACCCAGA ACGCGTTATC GGTGAATTGG CAGAGCATGG	5460
TGTGATGTCA ACTGCTTGGG GTGGAGATTC TGAATTTGTT GAAATTTCCG CTAAATTCAA	5520
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GGAAGAAGCT ATGAAAGGGA TGCTTGATCC AGAATTTGAA GAAAAAGTTA TTGCTGAAGC	6300
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CAACGGTAAG GTTGCCCGTG ACTCTAAAGT CCGTGTTATC CGTGATGGTG TCCTTATCTA	6420
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TCGTGAAGGT GGATTGATGA TCGACGCTA CAATGATATT AAGATGGATG ATGTGATTGA	6540
GGCGTATGTC ATGGAAGAAA TCAAGAGATA AGATTTTTC CTCCTTCTT AGGTGGTGAG	6600

1204

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CTGTGATGGG ACTGATAAAT CAGTTCCATC ACTTTCACCA CGGCGAAAGA AGCAGATGAC	6720
TTCAAATTGA ACTTCGTTTC AATTAACT GAAATCAAG AAGTTTAAAA TAGCTAGGTC	6780
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CAGATCGTGT GGGCATGGAA ATCAAGCGTG AAGTCAATGA GATTTTGCAA AAGAAAGTCC	6900
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TCGGGCTTGA AAAAGCAACT GGTACCATCA AACGTGAAC TGGTCGCAAT TTGAAATTGT	7080
ACAAAATCCC AGATTTGACC TTCGTCAAAG ACGAGTCCAT CGAGTATGGA AACAAGATTG	7140
ACGAGATGCT ACGCAATCTG GATAAGAACT AAAGAAGAGG GGTGCCCCCT CTTTTTGGT	7200
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AATAGTACGC CTCTACTTCT AAAATATTGT TAGAAATCGA TTTGACTGTC CTGATCGATT	7320
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TCCAAAAGAT ATTCCTACCT TATTGGAACA AGGTCCAACG ACTCTCTAT CTCAAGAAAT	7620
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TCTAGGCGTA ATGTTAGGGG TGAATGGAAC CGCTGCTTTG CTACGTGTTG GTAGTATAAC	7920
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CCCTATTTTG AAAAAAGTCT TAAAAATATT TGGTGTGAAT CTTACCAAGG GAGGGTTGGC	8040
CAAAGGAATG GGGAAATTTA TTCCTATCTT GGGTGGTATC ATTTTCAGGT GTTTAACCTT	8100
TGCAACTATG AAACCAATGG GGGAAAGCTT GCAGAAAGAA TTATCCAAGC TAGTCAACTA	8160
TAGTGAAAGT CAATATCAAG AAGATGTTGA AACAATCCGA AAAGAGGCTG AAATCATCAA	8220
AGGAGAGTAA TATGAATCCT ATCAAAGCTT TTGCTAAAAT TTATGGTAAT TACTTTTGA	8280
CCGTGCAAGG TGTAAGAGTG ATGAAAACGA TAAAGAAAGC TGACCATGTC GTTGTGGTC	8340
TGGGAAACT TTTTATTGCC GACAAGTTAA TGGATACGGC TCGGTGGCTC ATTAAGCCAG	8400

1205

AGGAGAGAGA ATGAAATTTT TTTGGTCTTC TTGCTATTCT TTTTATCAAA CCGATTATTG	8460
GGATTGTGAA ATTCCTTTTGG ATGATCATCT CTTTTGCAGT CCAATTGCTG TTTTACAAGA	8520
TAGTGTTTAA GATATTGGAT TGGCTCTTTA AACCTATCTA GATGGTAATC CAAGTTGCAG	8580
AGAACTAGCA GGAAGTCCAC TGCTAGTTTT TTATTCTCTT TCCATATGGT ATAATATAAG	8640
CAGTAAATC ATTTTATACT CTTCGAAAAT CTCTTCAAAC CACGTCAGCT TCACCTTGCA	8700
GTATATATGT TACTGACTTC GTCAGTTCTA TCCACAACCT CAAAACGGTG TTTTGAGCTG	8760
ACTTCGTCAG TTCTATCTAC AACCTCAAAA CACTGTTTTG AGCAACCTGC GGCTAGCTTC	8820
CTAGTTTGCT CTTTGATTTT CATTGAGTAT TAGAACATAC AATGGAGGTC GTCATGGACA	8880
ATATCATCGA TGTGTCAATT CCTGTGTCAG AAGTGGTGGA CAAGCATCCA GAAGTCTTGG	8940
AAATCTAGT GGAGTTGGGT TTAAACCCC TTGCCAATCC CTTAATGCGC AATACAGTTG	9000
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GATTCATATC CTACGGGATA TTTTGTTAGA ATTGACAAAT GGCGCCTCTC CTGAGTCGGT	9180
TCAAGATCGC TTTGATGCGA CCTTTACGGG CGTGTCAGCC ATCGAGATTT CCCTTATGGA	9240
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TCCGATTCGT AGATTGTTAG ATACCTATGA GTCTATGGAA GACGAGGAAA TGCTGGCGGA	9480
GATGCGTAAG GGTTTGGTGC GTCAGATGGG ACTTGTGGGT CAATTTGACA TCCATTACCA	9540
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CAAGTCACTA CCAGAAGTGT CAATTAGCAG TGTAAGGAA GCTTTTGAAG CTTTTCGCGC	9720
AGAGTTTGAA AGTATGATTT TCAAGGAAGA GTCCATCCTC CTCATGATTC TCCTTGAGTC	9780
TTTACTCAG GATGACTGGC TTCAGATTGC GGAGGAGAGC GATGCCTATG GCTATGCCAT	9840
CATCCGTCCG TCAGAGAAAT GGGTGCCAGA ACGACAGAGC TTTATTGAGG AAAAGATTGC	9900
AGAGGAGCCT GTACAGCTAG ATACGGCAGA AGGTCAAGTT CAACAAGTCA TAGATACGCC	9960
AGAAGGCCAT TTTACCATTA CCTTTACCCC TAAGGAAAAG GAAGCTGTGC TGGACCGCCA	10020
TAGTCAACAG GCTTTTGTA ATGGCTATCT TTCAGTCGAG CAGGCCAATC TCATCCTCAA	10080
TCATCTCCCT ATGGAGATTA CCTTGTCAA TAAAGAAGAT ATTTCCAGT ATTACAATGA	10140



1206

CAATACGCCA GCTGATGAGA TGATTTTCAA ACGGACGCCG TCCCAAGTCG GGCGCAATGT	10200
CGAACTCTGC CATCCGCCCTA AGTACTTGGA CAAGGTCAAA ACTATCATGA AGGGCCTTCG	10260
TGAGGGAAGC AAAGACAAGT ATGAAATGTG GTTCAAGTCT GAGTCGCGAG GTAAGTTTGT	10320
CCACATCACC TATGCTGCAG TACACGATGA AGACGGAGAA TTCCAAGGAG TGTTGGAGTA	10380
TGTTCAGGAT ATCCAGCCCT ACCGTGAGAT TGATACGGAC TATTTTCGTG GATTAGAATA	10440
AGGAGAAAAA ATGAGTTACG AACAAGAATT TATGAAGGAA TTTGAAGCTT GGGTCAATAC	10500
CCTAATCATG ATTAACGACA TGGCGCACAA GGAAGCCAA AAAGTTTACG AAGAAGACCA	10560
GGACGAGCGT GCCAAAGATG CCATGATTCG CTACGAGAGT CGCTTGGATG CTTATCAGTT	10620
CTTGCTTGGT AAGTTTGAAA ACTTCAAAGT AGGCAAGGGA TTCCATGATT TGCCAGAAGG	10680
CTTGTTTGGT GAGCGAAATT ATTAACGAG AAAGATTCTT GATTTTTCAC TAAAATCTTG	10740
ATAGAATGTT TATGTTAAAT CCTTGTCAGA GCAGGGA'TTT TTTATTGAAA GGATTTTATC	10800
ATGTCAAAGA AACTCAATCG TAAAAACAA TTACGAAATG GCCTCCGTCG CGCAGGTGCC	10860
TTTTCAGTA CGGTGACTAA GGTGTAGAT GAGACAAAAA AAGTCGTGAA GCGTGCAGAA	10920
CAGTCAGCAA GCGCAGCTGG TAAGGCTGTT TCTAAAAAAG TTGAACAAGC AGTAGAAGCT	10980
ACCAAAGAGC AAGCTCAAAA AGTAGCTAAT TCTGTAGAAG ATTTTGCAGC AAATTTGGGT	11040
GGACTTCCAC TTGATCGTGC CAAGACTTTC TATGATGAAG GAATCAAGTC TGCTTCAGAT	11100
TTCAAAAAC TGGACTGAAAA AGAACTCCTT GCCTTGAAAG GAATCGGCCC AGCTACCATC	11160
AAGAAATTGA AAGAAATGG CATCAAGTTC AAGTAATTTT TCTTGAGCCT TGCATTCCG	11220
AAAAAATCTT GCTACAATAG AGCCATTAGA GGTGTTTGA ATCCCACATT TTACAGAAAG	11280
TGGCGGCGCT GAGAAGTCCA CAAATGTGTC AAAACTGCTT GCTAATGGAT GAAAAATTGA	11340
AATAAAAGTG TCTTTTGCT TTAAAGACGA GAGTTGCG	11378

(2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4156 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CCGCGAGCCA CGCGGAATTT GCTGCGGTA TTCATCAGTC AGGATCTATG ATCTTTGGTG	60
AACAAGAAAA GGTTCAGTT GTGACCTTTA TGCCAAATGA AGGTCCTGAT GATCTATACG	120
CTAAGTTTAA TAACGCTGTT GCTGCATTTG ACGCAGAAGA TGAGGTTCTA GTTTTGGCTG	180

1207

ACCTTTGGAG TGGTTCTCCA TTAAACCAAG CTAGTCGCGT GATGGGAGAA AATCCTGAGC	240
GTAAGTTTGC CATCATCACA GGACTTAACT TACCGATGTT GATTCAAGCC TACACAGAGC	300
GCCTCATGGA CGCTGCTGCA GGTGTAGAAA AAGTCGCTGC TAATATCATT AAAGAAGCCA	360
AAGATGGCAT CAAAGCTCTT CCAGAAGAGC TAAATCCAGT CGAAGAAGTT GCAAGCGCTG	420
CAGCTGCTCC AGTTGCCCAA ACTGCTATCC CAGAAGGAAC TGTATATCGGA GACGGTAAAT	480
TGAAAATCAA TCTTGCCCGT CTTGACACAC GTCTACTTCA CGGTCAGGTT GCAACTGCTT	540
GGACTCCAGA TTCAAAAGCA AATCGTATCA TCGTTGCTTC AGATAACGTG GCTAAAGACG	600
ACCTTCGTAA AGAATTGATT AAACAAGCAG CTCCAGGTAA TGTCAAGGCT AACGTGGTTC	660
CAATTCAAAA ACTGATTGAG ATTTCAAAAG ACCCACGTTT TGGAGAAACA CATGCCCTTA	720
TCTTGTTTGA AACACCTCAA GATGCCCTTC GTGCCATCGA AGGCGGCGTG CCAATCAAGA	780
CTCTTAATGT TGGTTCTATG GCTCACTCAA CAGGTAAAC ATTGGTCAAT ACCGTTTGT	840
CTATGGACAA AGAAGACGTT GCTACATTTG AAAAAATGCG TGAATTGGT GTTGAATTTG	900
ATGTCCGTAA AGTACCAAAT GATTCTAAAA AAGATTTGTT TGAATTGATT AACAAAGCCA	960
ATGTCAAATA AGCCATTATT TATGAAAGGA TTTTAAACAT GTCTATTATT TCTATGGTTT	1020
TAGTAGTCGT TGTAGCCTTC TTTGCAGGTC TTGAAGGCAT CCTCGACCAG TTCCAATTC	1080
ACCAACCACT TGTAGCCTGT ACCCTTATTG GGCTTGTAAC AGGTCACTTG GAAGCAGGGA	1140
TTATCCTCGG TGGATCGCTT CAAATGATTG CCCTTGCTTG GTCAAATATC GGTGCTGCTA	1200
TCGCTCCTGA TGCTGCACTT GCTTCTGTCG CTGCTGCCAT TATCATGGTT CTGGTGGTG	1260
ACTTTACCAA GACTGGTATC GGTGTTGCCC AAGCGGTTGC TATCCCTCTT GCTGTAGCTG	1320
GACTTTTCTT GACAATGATT GTTCGTACAA TTTCAGTTGC TTTGGTTCAT ACTGCAGATG	1380
CTGCCGTAA AAAAGGTGAC TTCGGCGCTG TGGAGCGTGC GCATTTTCATC GCGCTACTTT	1440
TCCAAGGACT TCGTATCGCG CTTCTGTCAG CTCTTCTCCT TATGGTACCA ACTGAAACTG	1500
TACAAAGTAT CCTTAGTGCC ATGCCAGACT GGCTCAAAGA TGGTATGGCT ATCGGTGGTG	1560
GTATGGTCGT TGCCGTTGGT TACGCCATGG TTATCAACAT GATGGCAACT CGTGAAGTAT	1620
GGCCATTCTT CGCTCTTGGT TTCGTTCTCG CTGCTGTGTC AGATATTACT CTAATCGGAT	1680
TCGGTGCTAT CGGCGTTGCT ATCGCTCTTA TCTACCTTCA CCTTTCTAAA ACTGGTGGA	1740
ATGGTGGCGG AGGAGCCGCA ACTTCTAACG ACCCAATCGG CGATATCCTA GAAGACTACT	1800
AAGATAAGAA AGGACTGAAA ACATCATGAC TGAAAACTT CAATTAAC TAATCAGATCG	1860
TAAAAAAGTT TGGTGGCGTT CAACCTTCTT ACAAGGCTCT TGGAACCTTG AACGGATGCA	1920

1208

AAACTTGGGC TGGGCTTATA CACTCATTCC AGCTATCAAA AACTCTATA CTAAAAAGA	1980
AGATCAAAATC GCTGCTCTTG AGCGTCACCT TGAGTTCTTC AACACTCATC CATACGTAGC	2040
TGCTCCAGTC ATGGGGGTTA CTCTTGCGCT TGAAGAAGAA CGTGCTAACG GTGTGGAAAT	2100
CGATGACGCT GCTATCCAAG GGGTTAAAA CGGTATGATG GGACCTCTTG CTGGTATCGG	2160
TGACCCAGTA TTCTGGTTTA CAGTACGCCC AATCCTTGGA TCTCTCGGTG CTTCACTTGC	2220
CCTTACTGGC AATATCTTGG GGCCACTCCT CTTCTTTGTT GCATGGAACT TGATTCTGAT	2280
GTCATTCTTG TGGTATGTTT AAGAGATTGG ATACAAGGCT GGATCAGAAA TCACTAAAGA	2340
TATGTCTGGT GGTATCCTTC AAGATATCAC TAAAGGAGCT TCTATCCTTG GGATGTTTAT	2400
TCTTGCTGTC CTGTGTTCAAC GCTGGGTAAA TATTAAATTT GCTTTTCGATG TTTCTAAAGT	2460
TCAACTAGAT GAAAAGGCTT ATATCCATTG GGATAAAATG CCAGAAGGGT CTAAAGGTAT	2520
CCAAGAAGCA TTCGCACAAG TAGGACAAGG ATTGTCTCAA ACTCCTGAAA AAGTTACTAC	2580
TTTCCAACAA AACTTGGATA TGTGATTGCC TGGATTATCA GGACTACTCC TTACTTTACT	2640
TTGCATGTAC TTACTTAAGA AAAAAGTATC TCCAATCACT ATTATCCTTG CCCTCTTCGC	2700
AGTGGGTATT GTGGCACATG TTCTTCACAT CATGTAATCA AGCAACTAAA AAGGAACCAG	2760
GTTCTAAAAAT CTGATTCCTT TTTTCTATGC TTTTATTGAG CCAAGGCTCC CATTTGGATCC	2820
CATGGTGCAA GTACGATTGG TTCTGCTCCA TAGGCAGCTT GTTCTTCTGC TGTGAGCAAT	2880
TCCTTACGAA CAACGATTTG GTATGTGTAT TCGTCCATCC AAGCGTCTGA GGCAACAAG	2940
TAACCATCTG TACCGACCTT GTCTCCCAT GAGTTTCAA CCTTCCACTT GGTGATTTA	3000
CCATTTTCGT CCAAGTCAAC ACCTGTCAAG ACCATGGCGT GGGTCATCAA GCTTTCATA	3060
TAGTCCAAAC GTCCAGCCTT GTCTTGAGTA AGTTTAATGT CCATGCTTGA TTCAAAGTCA	3120
TAAACATCTG TCGCAAGGAT GCCAGCTTAC GGTGCTGAG CTGGCCGACA TCAGAACCAA	3180
ACCAAAACAGT CTCACCTGCT TGCATTTGGG CAATCGCCAA TTCTTTCAAG CGCTCCATTG	3240
GAACGTTGAT GTAGCGAAGT GCACGGCTAC CAACCACATT CCCCACATC TCAACTGTGT	3300
AAGATTTTCC GTAAGGTTTA TCAGCAGTTG GAGCATTGAT AACAGAAACG TAGTCTTCTA	3360
AAGGAAGATT GACATATTTT TTGTAAACT CTTGTGGTGT GATTCTTTT TCACTTTTGT	3420
AGTTGTTATC TTTATCCCGA TAAGCAAAGT CAACTTGCG TGGTGGAAGT CCTAATGACA	3480
TAGCAAGAAA GTTAAAGATT TCTTGCAAGA GGTCTTCTT CTTAGCTTGA ACAGTCGCTT	3540
GATCTGCACC AGAAACAAGC AAGTCACGCA AGATTTGAGC ATCTTGACGA AGCAATTTAT	3600
TAAGGATCGC ATTTAGCTCA CGACTGCTGC TAGATGAAAC AGACTCAGGA TAACTGACT	3660
TAGGCACGAC ACCGTATTTT TCAAAGAGGG AAACGACCAT ATCCCATTGA CCGCCATCTT	3720

1209

GTTGAGGTGT TTGGAGTAAG AAGCTAACTT GCGGCTAGTC AATTCTTGGT CTGAAGTCGC	3780
AATGACTTGC TCCAAGAACC AGTTTGATTT CTCATACTTA TCCCAGAAGA AAGTGTGGGC	3840
TTGTGACAAC TCAAAGTTCT CCAATTTGTA TTGCGAGATG AGTTTGTGGC GGAAGGTGTT	3900
GAGAGCCGCA AACATCCAGC AACGACCAGA CGCTTCTCTGG TTAGTGACCT TGTCTTGGT	3960
TAAATCCAAT GAGAAAACAG GTGTGTTGTC TACATGGCTT TGGCGACGTT CCAGAGCTGC	4020
AAAAATTCCG TTGTGGCTGG CAGCATTTC AATCGCTTGG TATTTTACAT TTGCTTCATA	4080
GTTGGCAAAT AGTTTATCAG TAAATGATTC TTGAATCGCG TTCATAGATT CCTCCTTTTA	4140
GTCTACAGTG TATTGG	4156

(2) INFORMATION FOR SEQ ID NO: 212:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3902 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

AAAAACAACA AATAAAACA AAAACAAAAA TATCGAGGTT TATTTTCAAA ACTTTCGATA	60
TTTTTATTAA GTTATTATTT TGTGTTTCT AGTTTACTTT TTGATGGTTA AGAGTGGTGG	120
AGAATTATAC TCAATGAAAA TCAAAGAGCA AACTAGGAAG CTAGCCCGAG GCTGTACTTG	180
ACTACGGCAA GCGGAAGCTG ACGTGGTTTG AATTTGATTT TCGAAGAGTA TTAGTGCAAA	240
CCGTAGTTGT AGTCATCATC TTGCATGGCT TCAACTTCGC CAAGAAGGTA ACCATTTCCG	300
ACTTGAGAGA AGAAGTCATG GTTGAAGTT CCTGTGAAA TACCGTTCAT AACGATTGGG	360
TTGACATCTT CAGCTGAATC TGGGAAAAGT GGATCTTGTC CCATGTTCAT GAGAGCTTTA	420
TTGGCATTTGT AGCGAAGGAA GGTTTTAACC TCTTCAGTCC AACCAACACC GTCATAAAGA	480
CTCTCTGTGT AGCCTTCTTC ATTTTCATAA AGAGTATAGA GTAGGTCGTA CATCCATTCT	540
TTGAGTTTTT CTGCTCTTC TTCAGGTAAT TCATTGAAAC CAAGTTGGAA TTTGTAACCA	600
ATGTAGGTTT CGTGAACAGA CTCGTCACGA ATAATCAATT TAATGATTTT TGCAACGTTG	660
GCAAGTTTGT TGTACCAGAG ATAGTAGAGG GGAGTGAAGA AACCAGAGTA GAAGAGGAAG	720
GTTTCGAGGA AGACGCTGGC AACTTCTTTT TCAAGTGGGC TGCCGTTTAG GTAGATTTCG	780
TTGACAATCT CAGCCTTCTT TTGTAGGTAA GGATTGGTAT TGGTCCATTC GAAAATTCTT	840
TCAATCTCAG CCTTAGTATT CAAGGTAGAA AAGATTGATG AGTAAGATTT AGCGTGGACA	900

1210

GATTCCATAA ATTGGATGTT ATTGAAGACA GCTTCCTCAT GTGGTGTACG GATGTCTGCG	960
CGAAGGGCTT GAACCCAGT TTCAGATTGC ATAGTGTCAA GAAGGGTTAA ACCACCAAAA	1020
ACTTTTCCGA CCAAGTCTTT CTCTTTGTTA GATAGCTTTC TCCAGTCATC CAAGTCGTTT	1080
GATAAGGGAA TACGTGTATC GAGCCAAAAT TGCTCCGTCA GTTTTTCCTCA AGTTGATTTG	1140
TCGATGACAT CTTCGATGGC ATTCCAGTTA ATGGCTTTGT AGTAAGTTTC CATTTAAAAT	1200
CTCTTCTGT GTTTAGTATT GCGAACTCAC AATTATTTCT ACTTTACCAT AATTCTATAG	1260
GAGTATCGCA CAAAAAGTCG GAAGCCCGAC TTTTAAAATG TTACATAAAT TATGTTATGA	1320
CATAGTAGAT TTGATTTTAT CAGTGCTGCT TAGGGAAAAA TAGTGTTTCT ATGCTAGAAA	1380
CTAAATCACA CAGCTTTCAC ATTGGTTGGC GCCGACTTCT CCACCGTCAT CTGTAAAGGT	1440
ACGGACGTAG TAGATAGACT TGATTCCTTT GTTAAAGCA TAGTTACGAA GGATGGACAA	1500
GTCACGTGTC GTTTGTTTAT TTTCCCTCTT CCATTCGTAA AGGCCTTTTG GAATGTCACT	1560
GCGCATGAAG AGGGTGAGTG AAAGTCCTTG ATCCACGTGT TCAGTCGCAG CAGCGTAAAC	1620
ATCGATGACT TTACGCATAT CCATATCGTA GGCAGAAGTG TAGTAAGGAA TGGTTTCTGT	1680
AGACAAGCCA GCAGCAGGGT AATAGATTTT ACCAATTTTC TTCTCTTGGC GTTCTTCGAT	1740
ACGTTGCGTA ATCGGGTGGA TAGAAGCAGA AACGTCGTG ATATAGCTGA TAGAACCATT	1800
TGGCGCTACA GCAAGGCGAT TTTGGTGGTA AAGACCATCT TCTTGAACCT TGTCGCGAAG	1860
TTACGCCCAA TCAGCAACAC CAGGGATAAA GACATTTTTC AAGAGTTCTT TAACACGGTC	1920
TGATGTTGGA ACAAATTCAC CAGTTACATA CTTGTCAAAG TAACTTCCGT TAGCATAGTC	1980
TGATTTTCA AAGTTGTGGA AGGTAATACC ACGTTCACGT GCAATATTGT TTGACTCTAC	2040
CAAGGTCCAG TAGTTCATAA GCATAAAGTA GATGCTTGTA AATTCAACAG ACTCAGGTGA	2100
ACCATATTCA ATGAGTTGTT GGGCAAGGTA GCTGTGCAGT CCCATGGCAC CGAGACCAAA	2160
GGTGTGGGCT TGGCTATTTT CATGGTCAAT CGTTGGTACA GCTACGATAT GTGAACATATC	2220
TGTAACGAAA GTAAGGGCAC GAACCATAGC ACGGATAGAA CGACCAAAAT CAGGTGAAGT	2280
CATCATGTTA ACCACGTTGG TTGAACCCAG GTTACATGAA ACATCTGTTC CCATTGAAG	2340
GAATTCCTGA GCATCGTTGA TCAAGCTTGG TTCTTGAAC TGAAGAATCT CAGAACACAA	2400
GTTACTCATG ATAATCTTTC CATCAACAGG ATTTGCACGG TTAGCCGTAT CGATGTTGAC	2460
TACATAAGGA TAGCCAGACT CTGTGTGCAA TTTAGAGATT TCAGTTTCCA AATCCCGCGC	2520
CTTGATTTTT GTCTTGCGAA TATTTGGATT TGCGACCAAT TCATCGTATT TTTCAGTAAT	2580
GTCGATGTAA TTGAATGGCA CACCGTATTC TTTTCTACA GAGTAAGGGC TGAAGAGGTA	2640
CATTCTTCA TTTTACGAG CCAATTCGTA GAATTTATCA GGTACTACAA CACCAAGTGA	2700

1211

TAGAGTCTTG ACACGTACTT TTTCATCAGC GTTTTCTTTC TTAGTTGAAA GGAAAGCGAT	2760
GATATCTGGG TGAAAGACGT TGAGGTAGAC AACACCAGCA CCTTGACGTT GCCCCAATTG	2820
GTTGGAGTAA GAGAAGCTGT CTTCAAAAAG CTTCATAACA GGAACGACAC CTGAAGCAGC	2880
TCCTTCATAG CCTTTGATAG GTGCACCAGC TTCACGAAGG TTGCTGAGGG TAATTCCCAC	2940
ACCACCACCA ATACGTGAAA GTTGAAGAGC TGAGTTGATA GAACGCCCGA TAGAGTTCAT	3000
ATCATCCGTC ACTTGGATTA GGAAACAAGA TACCAACTCC CCACGACGAG CACGTCCAGC	3060
ATTCAAGAAG GAAGGAGTAG CAGGTTGGTA GCGTTGGTGG ATGATTTCAT TGGCAATATC	3120
GATTGCAACA GCTTCATTCC CATCAGCGAA ATAAAGGGCA TTGAAGAAGA CACGGTCTTC	3180
CATATTTTCA AGATAGTATT CACCGTCATT AGTCTTTAAG GCATATTGAT TGTAAAATTT	3240
ATAAGCTGCC ATGAATGACT TGAATTGGAA GTTTTGGTCT TTGATAAATT GAGCTAATTC	3300
TTCCAAGAAC TCTGGACGGT ATTTCTTGAT AAAGGCTGTT TCGATGTAGT TGTGTTCAAT	3360
GAGGTAATG ATTTTGCTCT TGATTGAATC AAAAACCATA GTGTTTGGAA CTACATTTTC	3420
TTTAAAGAAA GCATCCAAGG CTTCTTGTC TTTATGAAGC ATGATTGTGC CATTAAACAGG	3480
ACGGTTAATT TCGTTATTAA GACGGAAGTA AGTCACGTCT TCAAGATGTT TTAATCCCAT	3540
AAAAATTTCCC TTATCTAATT ACAAAGAAA GGCTTCTAAG TTAGCCCTAA AAGCAGTTTC	3600
TTCTGGATGA TGIACAAAGA TTATGCTAAT TGTTCAGTT TTTCTGGTTG GAAACCTGAA	3660
AAGACTTCAG TTGGTGTTTG GATAACAGGA GCTGCGCTAA AACCGAGCTC TTAACTTGA	3720
TCGAGCTACT CAGGTGCTC ATCAAGATTG ATTTACGAT AAGAGACATT ATTACTGTCC	3780
AAGAAACGCT TGGTCATTTT ACATTGGACA CAATTGTTTT TAGAATAAAC GGTTACCATT	3840
GTGTAACCTC TCTTCAAAAT TTAATACTAT CTTAGTATAT CAGAAAATAA AATTTTGTCTG	3900
GG	3902

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2456 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TATTGAAGCT ATTGTAGACT ACAAAGATAA GGATTTGCAG TTAGTAGGCG GTGAGACTCA	60
CTGATAACCT AAAAAGGATA GTCAATTATG CTTGTTTACT AACTATTAAC TATGCTAAAT	120

1212

CAATTGAGGT TGTTCACATA AAACCTCTATA TCAGAGAAGC CTGATATAGA GTTTTTTCTT	180
GCTAGTTTTA GGATTTTTTT GTAAAATAGA AAAAGTGAAG AGAGGTATGA AATGAGCAAG	240
AAAGATAAAA AAATCGAAAT TCAAGTAGCG GATGCCAAAG TTAATGTTGG TAAAGACAGT	300
TTTGAAGGTT ATACATTGAC TATCGGTAAA AAAGTTATCG GAGAAATTGC CGAATTAGAC	360
GGACAATTTG CCATTATAAA GAATGGGAAT GTCGATAGTT TTTATAAAAA ATTGGAAAAA	420
GCTGTGGA AAA TTTTGATTGA AAATTATAAT TTAGCAAAAT AAGTCTTGT TTTTGGAAAT	480
TTTCATGATA TAATAGTCCA TGTGATTGT AGGAGAGATA GCGAAGAGGC TAAACGCGGC	540
GGACTGTAAA TCCGCCCTT CGGGTTCGGG GGTTCGAATC CCTCTCTCTC CATTTCATTA	600
ATGGGGTATA GCCAAGCGGT AAGGCAAGGG ACTTTGACTC CCTCATGCGT TGGTTCGAAT	660
CCAGTACCC CAGTTCCTAG GTAATAATCA AGATAGAAAG CAAAATATCT TAGGGTATTT	720
TATTTTATA ATTGAAAGAC GTGAATGATA TGAACATGTC CTGCGGGTG CTTAGGAAAA	780
AAATTATAAG TATGTCAAGT TTAAGAAAAA CTTGATTGTT GGAGGATTTT TTAGATGAAC	840
GAATTGAAG ATTTGCTAAA TAGCGTAGT CAAGTTGAGA CTGGTGATGT TGTTAGTGCT	900
GAATATTGA CAGTTGATGC GACTCAAGCT AACGTTGCAA TCTCTGGAAC TGGTGTGAA	960
GGTGCTTGA CTCTTCGCGA ATTGACAAAC GATCGTGATG CAGATATCAA TGACTTTGTT	1020
AAAGTAGGAG AAGTATTGGA TGTCTTGTA CTTCGTCAAG TAGTTGGTAA AGATACTGAT	1080
ACAGTTACAT ACCTTGATC TAAAAACGC CTTGAAGCTC GCAAAGCATG GGACAACTT	1140
GTTGGTCGCG AAGAAGAGT TGTACTGTT AAAGGAACGC GTGCCGTAA AGGTGGACTT	1200
TCAGTAGAAT TTGAAGGTGT TCGTGGATTT ATCCCAGCTT CAATGTTGGA TACTCGTTTC	1260
GTACGTAACG CTGAGCGTTT TGTAGGTCAA GAATTTGATA CTAATAATCAA AGAAGTTAAC	1320
GCTAAAGAAA ACCGCTTCAT CCTTTCACGT CGTGAAGTTG TTGAAGCAGC TACTGCAGCA	1380
GCTCGCGCTG AAGTATTCGG TAAATTGGCT GTTGGTGATG TTGTAAGTGG TAAAGTTGCT	1440
CGTATCACAA GCTTCGCGC TTTCGTCGAC CTTGGTGGTG TTGACGGATT GGTTCACCTG	1500
ACTGAATTGT CACATGAACG TAATGTATCA CAAAATCAG TTGTAAGTGT TGGTGAAGAA	1560
ATTGAAGTGA AAATCCTTGA TCTTAACGAA GAAGAAGGAC GTGTATCACT TTCACTTAAA	1620
GCAACAGTAC CAGGACCATG GGATGGCGTT GAGCAAAAAT TGGCTAAAGG TGATGTAGTA	1680
GAAGGAACAG TTAAACGTTT GACTGACTTC GGTGCATTG TTGAAGTATT GCCAGGTATC	1740
GATGGACTTG TTCACGTATC ACAAATTCA CACAAACGGA TTGAAAATCC AAAAGAAGCT	1800
CTTAAAGTTG GTCAAGAAGT TCAAGTTAAA GTTCTTGAAG TTAACGCAGA TGCAGAACGC	1860
GTGTCACTTT CTATTAAAGC TCTTGAAGAA CGTCCAGCCC AAGAAGAAGG AAAAAAGAA	1920

1213

GAAAAACGTG CTGCTCGTCC ACGTCGTCCA AGACGTCAAG AAAAGCGTGA TTTCGAACTT	1980
CCAGAAACAC AAACAGGATT TTCAATGGCT GATTGTGTTG GTGATATCGA ACTTTAATCA	2040
AATTGAAAAT TCACAAAATC CTTTGTGTAC TAAACAAGGG ATTTTCTCGG CTCTTTGTCA	2100
ACTGTAGTGG GTTGAAGAAA AGCTAAGCTC GAGAAAGGAC AAATTTGTTC CTTTCTTTTT	2160
TGATATTCAG AGCGATAAAA ATCCGTTTTT TGAACTTTTC AAAGTTCCGA AAACCAAAGG	2220
CATTGCGCTT GATAAGTTTG ATGAGATTAT TGGTCGCTTC CAGTTTGGCG TTAGAATAGT	2280
GTAGTTGAAG GGTGTTGACA AGCTTTTCTT TATCTTTGAG GAAGGTTTTC AAGACAGTCT	2340
GAAAAATAGG ATGAACCTGC TTAAGATTGT CCTCAATAAG TCCGAAAAAT TTCTCCGGTT	2400
CCTTATTCTG AAAGTGAAAC AGCAAGAGTT GATAGAGCTG ATAGTGGTGT TTCAGG	2456

(2) INFORMATION FOR SEQ ID NO: 214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10974 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

AAATAGGATA TAGAGACATC CTTCTGATCT GCTTTTtWACA AAGTCCAATT ATATGCGGAT	60
CTATACCTCC ACAATGTCCA TTATTATmCC TAACTATAAT ATGAGCCGAA AACACTATAT	120
CCTTAATGTC TCCATATCCA TCAGGGATAT TAATATTTAT TTTTCCACAA CTATATTGCA	180
TTGTAACCAT CTCCTTAAAC GACGCATTAT GATATTTGAT AGAGAAATTT TTATGAATAA	240
CTCAATAAAT TTATAGTAAA TCATGCTTAT ATCTCAAAGA TACCTATTTT ATCTTGCTCTC	300
GACCTTCTCC AAAGAATTGC TATAATACTA TTACAAATCC ATCTGCACTA CACTTCAAAT	360
TTTAGCACTG TATAAAAACG TTTCAATACA CTAAC TTCAA GAAAAC TTCC ACTATTAATT	420
GAAAAAATG ATAGAGATAA ATTAAAAATC TATATTGAAA CTCATCCCGA TGCTTATTTG	480
ACTGAAATAG CTGCTGAATT CAACTGTCCT CCAACAAC TA TCATTACGC TCTAAAGGCT	540
ATGGGATATA GTCTAAAAAA GAGCCGTACC TACTGCGAAC AAGACCCAGA AAAAGTAAAT	600
CGGTTCCCTTA AAGAATTGAA TCACTTAAGC TACCTGACTC CTATTTATAT TTATGAGACA	660
GGGGTTGAGA CCTATTTTTA TCTCGAATAT GATCGAGCCT TGAGCAGGCA GTTAGTCTCT	720
CTGGAAGAAG ATATAATTAT TTGAATTAAG ATCGAGACAA CGCACACCAG AGATTGCGAT	780
ACTGTTATAG AAGTACTAAT GCCCTTTTTT GTTCAATAT ACTATGGCTC CGATGACCTA	840



1214

TAAAGATACG ATGACGAGTG ACTTTTTCGA AGCTTGCTTC CAAAAATTCT TACTACCTAC	900
TTTAGATACA CCATCCCTTA TCATTATGGA CAATGCAAGG TTTACAGAA TGAACATGTG	960
TAAGGAGCAG GGCATAGACT GTTACCACTT CCTACCTATT CACCCGAGTA TAATCCCAT	1020
GAGAAAATAT GGGCTTACAT CAAAAACATC TCAGAATAAT ATTGTCAAAT TACGATGCTT	1080
TTCTTGAGGC ACTTTTGTCC TATTCTTGTT TCAGCCGACT ATACTCCGTT ATTGGGCAGC	1140
TACGGAACAG TCGATGGGAC GATGGGGGGA CATAAAAAA TCCTCCAGTT TTGTTTTTTA	1200
TAACAGTATA CTGGAGAATT GACAATCTCG GTAGATACCT CGTTATAGCG CGGTTACTTA	1260
TTAGCCAGTT ACAAACAAC TGTGAACAGA AACATTTCCA GAGTCAGACA AGACTTTGGA	1320
ATGTTTTGGC TCTATAATTT CTGTAGTGGG TAATCCCACC CCAGGAATTGA TAGGGTCGTT	1380
TCTTGTAGAA AAAAAGCCCC ATATGACCTA TAATGAAAAG CGTCTAACCA ACTCATTAGA	1440
AAGGGTTCAT ATGGAACAAC TTAAGAATAC CACAGATTG CTCGGATTGG AAGACAAAAA	1500
TATCAAAATC TTGTCTGTTC TGAAATACCA AACCCATCTA GTCGTTACAG CAAAGTTGGA	1560
TTCCCCGCT CCTCCTTGTC CTCATTGTCA AGGGAAGATG ATCAAATACG ACTTCCAGAA	1620
AGCCTCTAAA ATTCGCTTC TCGACTGTCA GGGTTTACCC ACGGTACTGC ATCTCAAAAA	1680
GCGCCGCTTT CAGTGCAAGA ATTGCCCTAA GGTGGTCGTT TCTCAAACAT CCATTGTCAA	1740
GAAAAATTGC CAGATTTCGA ACATGGTGAG ACAAAAAATC GCTCAGCTCC TCCTTGAAAA	1800
GCAGTCTATG ACTGAGATTG CCCACAGATT GCGGCTCTCA ACTTCCACCG TCATCCGAAA	1860
ACTGAGGGAA TTTAAGTTTG AALCCGATTG GACCAAGTTG CCAAAAGTTA TGAGTTGGGA	1920
TGAGTATAGC TTCAAAAAGA GCAAAATGAG CTTCATTGCC CAAGATTTTG AGTCCAAATC	1980
CATCCTCGCA ATTTTAGACG GCGAACTCA TCGGCTGATT CGAAACCATT TCCAACGCTA	2040
TCAGAGAGAG GTTCGGGAGC TGGTCGAGGT CATCACCATG GACATGTACA GCCCTTATTA	2100
TCGGCTCGCT AAGCAACTCT TTCCAAAGGC GAAGATTGTT CTTGACCGCT TCCACATTGT	2160
CCAAATCTG AGCCGAGCTA TGAACCGAGT ACGAATCCAA ATCATGAACC AATTGACCG	2220
AAATCCTTG GAGTATCGGG CGCTCAAGCG CTTTGGGAAC CCTCGCTTTT TCGTTTCTAG	2280
GCTCGGGCTA AATCAGTCCA CTGGACTGAT TTACTIONACC AGTATAGCTT CAAGCTCTGT	2340
CAGAAACGAT TCTATCAGCC CACGTTTCGA ATGCACCTAA CCCATCGGGA AGTACGAGAT	2400
AAGCTGCTTT CTTACTCTGA GGGATTACAG GTTCACTACG AACTCTATCA ACTCTGCTC	2460
TTTCATTTTC AAGAGAAGAA TGCCGACCAT TTCTTTGGAT TGATTGAGCA AGAACTGCCA	2520
ACGGTTCATC CGCTTTTTC AACGGTCTTT TGGACTTTTT TAAGGGATAG AGATAAGATT	2580
ATCAACGCAC TTAAGCTGCC TTATTCCAAC GCTAAACTTG AAGCGACCAA TAATTTGATT	2640

1215

AAGATTATCA AGCGCAAAGC CTTTGGTTTC CGGAACCTTA ACAATTTTAA AAAACGGATT	2700
TTGATGACTT TGAACATCAA AAAAGAGAGT ACGAATTTTC TACTCTCCAG ATTGCAGCTT	2760
TTCGCCTACC CACTACACTT GACAAAGAGC CACTCTTTAT TCCATGGTAT CAAAGGCAAG	2820
ACTTGGTTTG GCATTGAGGT CCCAGCCTGC GAAGTTTCTT TTGTTCCTACT CGCTGACGCT	2880
GGCATAGGCA ATCATACCTG CATGTCTCC GCAGAGTCGC AGAGGGGGGA TGATAACCTT	2940
GACATCTGTG ATTTCCGGCTG CTAGGCGTTC TCTGAGACCT TTATTGGCTG CCACACCACC	3000
TGCCACAAC T AGGATTTTAA CAGGATATTT CTCCAAGCC TTCTTGGTTT TTGCCATGAG	3060
AATGTCCATA ACTGTGCTT GGAAGGAAGC ACACAATCT TCTGTAGACA GGCTTTCTCC	3120
CTTTTGCTCG GCATTGTGAT GAAGATTGAT AAAGGCAGAT TTCAAACCTG AGAAGGAGAA	3180
CTCCAGATTA TCTTCCTTAA TCATGGCAGC GGGGAAATCA TAAATATCCT GCCCCTGATG	3240
AGCCAGCTCG TCAATCTCAC GACCTGCAGG ATAGGTCAAG CCCATGACAC GGCCGACCTT	3300
ATCATAAGCC TCACCAACCG CATCATCACG GGTTCCTCCA ACAATCTTAT AATCTCCTGC	3360
CTCCGAAACA TAAACCAACT CTGTGTGTCC GCCGTGACC AAGAGGGCTA GCAAGGGAAA	3420
CTCCAAAGGC TCCCACTCT GAGCTGCCAT GAGGTGCCCA GCCATGTGAT TAACAGGAAT	3480
CAGTGGAAGT CCGTGAGCCC AAGCAAAGGC CTTGGCAGCT GACAAACCAA CTAGCAAGGC	3540
TCCGACCAAG CCTGTCCGT AGGTAACCGC AACAGCTGTC ACGTCCTCTT CGGTAATCCC	3600
TGCTTCTGCC AATGCCTCCT CGATACAGGC TGTAATGACC TCGACATGGT GACGACTGGC	3660
TACTTCGGGC ACTACGCCAC CAAAACGTTT GTGACTCTCA ATTTGACTAG CAATGACATT	3720
GGACAAGAGC TCATCGTCGT TTTTCAAGAC GCGGACACTG GTCTCATCAC AGGATGTCTC	3780
AAATGCTAAA ATATATCTAT CCTTCATCTA TTTCTCTCTT CATGATAATG GCGTCCTCGA	3840
CTGGGTCATG GTAGTAGGCC TTTGCTCAG CGATAACTGT CATCTTTTCT TTCTTGTAAG	3900
ATGCTTGCGC TCGTTGATTT GACTGTCTGA CTTGAGGAA AATTTCCTTG TCTGTCGGCA	3960
ATTGAGCAA CAAGGCTGAC GCAATCCCCT GACCCTGATA AGCTCCTTG ACAGCGATTT	4020
GCAGGACTTC TGCTTCAAAA AGATTCTCCT GCACAGCTAG AAATCCAATC ACTTCTGCCC	4080
CATCATAAGC CAATGCATAC CAAGTCTGGT CTTGGGACAG ATCTGCTTGG ATTTGCTCCA	4140
GAGTCCAAGG ACTGACTAGG TAAACAGCTG CCATAACAGC GTAGATGGCT TGAGCTAGGT	4200
CAGGCTGTTG TTGAATTCGC TTGATTTCTA TCATAGGCGT TTAATGTAAG ACTCGCCAGA	4260
CTCGGTATGG TTCTTGAGCC AGTTTTCCTC AGCCTCGACT CGTTTGAGGT AATTCGGCAC	4320
AAAATCATGC AAGGAGTCTG CTTCTTGTC CCAGGCCAAA AGAGCTAGAT TAGCTGCATT	4380

1216

GGGCAATGTT TCTTTGTAAT CAGTCCTTGG CAAGTGTTTT TGAATCTGCT CAACAAAGGG	4440
GCCAACTTCT CCGACAAAGG TTACCTGACT AGTACCCTTG ACTTTTCTTA GCACCTCTTC	4500
AAAAGATAGG TGCCTTCTG CCATGACAGG TTTGGCATT TCATAAAATC CTGCATAAAC	4560
ATTATTGCGA CGCGCATCCA TCAAGGGGAC AAACAAACCT TCTTGTGAT GGGGCACCAG	4620
AGCCAAGAGA CTCGACATAC CAACCAACTC GATGTTGAG GTGTGAGCTA AGGTCTTAGC	4680
AGTTGCTACC GCAATTCGCA AGCCTGTATA GCTACCCGGC CCTTCAGCTA CCACGATTCTG	4740
GTCCAAATCC TTGGGTGTCC AATCCAACT TGCCATCAAA AAATCGATGG CAGGCATAAG	4800
AGTAATACTG TGATTTTCT TAATATTAAT CGTCGTCTCG GCAAGAACCT GCTTATCCTC	4860
TAAATAGCC AGAGAAAGAG CCTTGCTGGA CGTATCAAAA GCTAATACTT TCATAACACA	4920
TTCCCTATCTT TTTGTCTGCT TACTATTATA CTACAAAAGC TGGCACATGG CAATTTTCTT	4980
TGCCCCAGA CAAGAGTGCC CTCACTTAAC TAAAAATAAT TAAAAAAAT GCTCACTTTT	5040
CCTTTTCTTT TCCGAATATA AAAGTGAACA AGAAAAAGG AGGAAAGTTC AATGACAAAT	5100
TTTGACATTC TTGACAATCA ATTTTATCC TTATCTGAAA ATGAATTATC AGATATTGAT	5160
GGCGGTCTCG CTCCTTGGT TATCTTTGGA GTAGCAGTAT CTGGGAAGGC TATTGCAGGT	5220
GGAACAGCAC TTATAGGTTT TGGTTTGCA GCTGTTATT TTTTAGGAGG AGATTAATAT	5280
GATGAAAGAT TTGAACAATT ATCGTGAAAT TTCTAATAAG GAATTGCAAG AAATCAAGGG	5340
TGGCTTTGGT GTCGGTGTG GTATCGCTTT ATTTATGGCA GGTATATACCA TTGGAAGA	5400
CCTTCGTAAT AAGTTTGGTA AGTCATGCTA GATAAGAAAC ACATTTTATAG AAGGATAAAT	5460
TTTATTGTCT TCATCTCTTA CAGTTTGCTC AGCATTCTCA ATGATTGAA CATTACTACC	5520
ATCCCTTTAC CATTCGATTT ATCTGTTTGT ATTGTTTAT TTTTATGCTT CAACTCTATT	5580
TTTGATCAGA ACAATGACTC CCATAAAAT AATAAGCTTT GAAAATCCA TTGTCATGTC	5640
ATGTTAGAAA AATGCAAAGA CCACCTCATC TTGATAGATG GGGTGGAATT TTCGTGTCGT	5700
AAATCTACTA TCTCTACATT CCCAAACAAA AAACCCAGC ATAAGCAGGG CATCTAAGCA	5760
TTTAATTCAA AGTAAATAC AAACCAACG ACATAGGTCA CGAGGAGGAG AAAAAGCGAG	5820
TAGAGAGTCA CAAAGGTCA TTTCCACAAG AACTTGGTTT GTCGTGCTC CAGTTTGGCA	5880
AATAGAAGAT TCCCCGATA AACGCAAGCA ACAAAAACAA TAAAAGCTAC CAAGCGAGCT	5940
CCGATAGCAA AAGCAAATAA GTTATACATA GGGCAACCTC CTTGACTTAA AATCTATATG	6000
GAATTATGAC AAGCAATAAA TTTCACTTCC GTTATCAACA TAATACATT TCTTTATTTT	6060
TGAAAACGCT TACCAAAGAA ATCGTCCCCT AACTTTCTCG TTTCCGTCTT TTACTAATTT	6120
TTCA'TTTTGT GGTATAATTG AAATAATTGT AACGAATCAA GGTCAATCTA GACACAAAT	6180

1217

GGAATGAAAT CAAGCAAATA TCTGCTAAAA GTTTGGAATA AGCTGACCTG TAAATAGAAA	6240
GGAACATATAT GATTTACAAA GTTTTTTATC AAGAAACAAA AGAACGTAGC CCACGCCGTG	6300
AAACAACACG CACGCTTTAC CTAGACATCG ATGCCAGCTC AGAACTTGAG GGCCGTATCA	6360
CTGCTCGCCA ACTTGTCGAA GAAAATCGCC CAGAGTACAA TATCGAGTAT ATCGAACTCT	6420
TGTCTGACAA ATTGCTCGAT TACGAAAAAG AAACCTGGCGC CTTCGAAATT ACGGAGTTCT	6480
AATATGGCCT ACACTCTTAA ACCTGAAGAA GTCGGCGTTT TTGCCATCGG TGGTCTAGGA	6540
GAAATCGGGA AAAACACTTA CGGAATTGAA TACCAAGACG AGATTATCAT CGTCGATGCT	6600
GGGATTAAAT TCCCAGAAGA TGACTTGCTT GGTATCGACT ATGTCATTCC TGACTACTCT	6660
TACATCGTGG ACAATATCGA CCGCGTCAAG GCTGTTTAA TCACACACGG ACACGAGGAC	6720
CACATTTGGTG GGATTCGGT CTTACTCAAG CAAGCAAATG TCCCTATTTA TGCTGGACCG	6780
CTTGCCCTGG CTTTGATCCG TGGGAACTC GAAGAACACG GCCTCTTGCG CAACGCCAAA	6840
CTTTACGAAA TCAACCACAA CACCGAGTTG ACCTTTAAAA ATCTCAAGGC AACTTCTTT	6900
AGAACGACTC ACTCTATTCC AGAGCCTTTG GGGATTGTCA TTCATACTCC TCAAGGGAAA	6960
ATCGTCTGTA CGGGTGACTT TAAGTTCGAC TTTACTCCAG TTGGAGAACC TGCGGACTTG	7020
CATCGTATGG CTGCGCTTGG TGAAGAAGGC GTGCTCTGTC TCCTGTCTGA CTCGACAAAT	7080
GCGGAAGTAC CAACCTTTAC CAACTCTGAA AAAGTCGTTG GTCAGTCCAT TATGAAGATT	7140
ATCCAAGGTA TTGAAGGACG TATCATCTTT GCATCCTTTG CCTCAAATAT CTTCCGTCTC	7200
CAGCAGGCAA CAGAAGCTGC TGTTAAGACT GGACGCAAGA TTGCGGTCTT TGGTCTTCT	7260
ATGGAAAAGG CCATTGTCAA CGGAATCGAT CTTGGCTACA TCAAAGCTCC TAAGGGAACC	7320
TTTATCGAGC CAAATGAAAT CAAAGATTAT CCTGCAGGAG AAGTTCTTAT CCTCTGTACA	7380
GGTAGTCAGG GTGAGCCTAT GGCAGCCCTC TCTCGTATCG CCAACGGAAC CCACCGTCAA	7440
GTACAATTAC AACCAGGTGA TACCGTTATC TTCTCTTCTA GTCCCATCCC TGGAACACT	7500
ACTAGTGTCA ACAAGCTGAT TAACATCATT TCTGAAGCTG GTGTCGAAGT TATCCACGGT	7560
AAAGTGAACA ATATCCATAC ATCTGGACAC GGTGGTCAGC AAGAGCAAAA ACTCATGCTC	7620
TGCTTGATTA AGCCAAAATA CTTTCATGCCT GTCCACGGTG AATACCGCAT GCAAAAAGTC	7680
CACGCTGGAC TAGCAGTGGA TACTGGTGTT GAGAAGGACA ATATCTTTAT CATGAGCAAT	7740
GGCGATGTGC TTGCCCTTAC TGCTGACTCA GCTCGTATCG CAGGTCATTT CAACGCCCAA	7800
GATATCTATG TCGATGAAA TCGTATCGGT GAAATTGGCG CAGCTGTCCT CAAAGATCGT	7860
CGCGATCTAT CTGAAGACGG TGTCGTTCTG GCAGTTGCAA CTGTTGACTT CAAATCGCAG	7920

1218

ATGATTCTAT CTGGTCCAGA CATCCTCAGC CGAGGCTTTG TCTACATGAG AGAGTCTGGC	7980
GACTTGATTG GCCAAAGCCA GCGTATCCTC TTCAATGCCA TTCGTATCGC ACTGAAAAAT	8040
AAGGATGCTA GCGTGCAATC TGTCAATGGT GCCATTGTCA ACGCTATTTC CCCCTTCCTC	8100
TATGAAAAATA CCGAACGTGA ACCGATCATC ATCCCGATGA TCCTCACACC AGATGAAGAA	8160
TAAAGCAAGA AAACAGCCCC GTCCTCGGAG CTGTTTTTCT CTATGCTTTC TTTTGAGATT	8220
AAAACTCATA CTCAATGAAA ATCAAAGAGC AACTAGGAA GCTAGCCGTA GGTTGCTCAA	8280
AGCACTGCTT TGAGGTGTGA GATAGAACTG ACGAAGTCAG TAGCCATACC TACGGCAAGG	8340
CGACGTTGAC GCGGTTTGAA GAGATTTTCG AAGAGTATCA ATAAAAATCG AAATCAGACT	8400
AGAAGGCTAA GCGAAAGCAT AACTTGAGTT AGCTCCCATG GTTCGGGAAA CTATGGGAGG	8460
CTGGAGATGA ATCAAAGCCA AGCTTTGAAC TCATTGTAAG GAAGCCGACG ACGTATCATT	8520
TTGATTTTGT AAGAGTTTTA GAAATACTAC GATTTTTACC TTCCAGATAC ACCATCAAAA	8580
TAGAAATATC TGCTGGGTTT ACTCCCGAAA TACGGCTGGC TTGGCCGATG GTTCTGGAT	8640
TGATGAGTTT GAACTTCTGA CCGGCTTCGG TTGCGATAGA ATCAATGTCA TCCCAGTCGA	8700
TATTGGCCCG AATGCGTTT TCTTCCATGC GTTTCATCTT GGCAACCTGG TCCATGGCTT	8760
TGGAATATA GCCTTCATAC TTGATTCTG TTTCAATCAA TTCGATAATC TTGTCATCCA	8820
AGTCTTCTGC AGCTGGTCCG ATGAAGGCCA CCACATCTTG GTAAGAAACT TCTGGACGGC	8880
GAAGGAATTC CTTGGCTGTC ACTGCATCGG TCAAGGGTTT GAAGCCCATC TCCTCAACCT	8940
TGGCATTGGT TTCTTGACT GGCTTGAGTT TGATACTGTC TAGGCGCTTC ATCTCATTAT	9000
CAAAATTGATT TTTCTTGATT TCAAAACGAG CCCAGCGTTC ATCGTCCACA AGGCCAATCT	9060
CGCGTCCCAT CTCAGTCAAG CGCATATCAG CATTGTCTAG ACGAAGAATG AGACGGTATT	9120
CAGCACGACT GGTCAAGAGA CCGTAGGGTT CAATGGTTCC CTTGGTCACC AAGTCGTCGA	9180
TCATCACCCC GATATAACCA TCACTGCGCT TCAAAATCAA TTCAGGCTTG CCTTGGAATT	9240
TCAGAGCCGC ATTGATACCC GCGATAATCC CTTGGCCTGC TGCCTCTTCG TAACCTGATG	9300
TTCCATTTGT CTGACCAGCA GTGAAGAGAC CTGAGATTTT CTTGGTTTCC AAAGTCGCAC	9360
GCAACTGATG AGGCAAGACC ATATCATACT CAATAGCATA ACCTGTCCGC ATCATCTCTG	9420
CATTTTCCAA ACCTTTGATG GAATGCACCA AGTCACGCTG GACATCCTCA GGCAGACTGG	9480
TTGAAAGTCC TTGCACATAG ACTTCCTCAG TATTGCGCCC TTCTGGCTCA AGGAAGAGTT	9540
GGTGACGTTT CTTGTCCGCA AAGCGACAA TCTTGCTCTC AATCGACGGA CAGTAACGAG	9600
GCCCCACTCC CTTGACCACA CCTGTAAACA TAGGCGCAGG GTGGAGGTTG TTTTGATAA	9660
TCTCATGACT GGTACCATTG GTATAGGTCA ACCAGCATGG TACTTGGTCC TTGACATAAT	9720

1219

CCTCATCAGC TGAAGTGTAT GAGAAATGAT TAGGCACCTC GTCTCCTGGC TGAATTTCTG	9780
TCACATCGTA ATTGATAGAA GAAGCCTTGA CACGTGGAGG GGTTCCTGTC TTGAAACGAC	9840
CGATTTGAG ACCCAGTTCC TTGAGATTGT CAGCTAGGTT AATAGAAGCC AAGCTGTGGT	9900
TAGGACCTGA TGAGTACTTG AGGTCTCCGA TGATAATTTC CCCACGGAGA GCAGTCCCTG	9960
TCGTCACAAT AACAGCCTTA GCAGCATATT CTTGATGGGT GGCTGTACGC ACACCGACAA	10020
CCTTGCCATC TTCCACCAAA ATCTCATCAA TCATGGTTTG ACGAAGGGTC AGATTTTCTT	10080
GGTTTTCAAC CGTCTTGGCG ATCTCCCTAG AGTAAAGTTC CTTGTACGCC TGCGCACGAA	10140
GGGCACGGAC AGCTGGCCCC TTCCCTGTGT TTAGCATCTT CATCTGGATG TAAGTCTGT	10200
CAATGGTTTT GGCCATCTCG CCACCGAGGG CATCGACTTC ACGCACGACA ATCCCCTTGG	10260
CAGAACCACC GATAGAGGGA TTACAAGGCA TGAAAGCCAG CATTTCAATA TTGATGGTCG	10320
CAAGCAGGAC CTTACAGCCC ATACGGCTAG CGGCCAAGGA AGCCTCAACC CCAGCGTGT	10380
CCGCACCAAT TACAATAATA TCGTATTCTT CAGTAAAATG ATAAGTCATG TTTCTCTCCT	10440
ATTCCTCAAG ATGAATGTGT CTTAGTTGGC CTTCCCAATC TGGTAGGGCT GTTTTTAAAA	10500
AGACTGGAAC TAGCTGGATA TTCTGGAGCT TATCCAAGTC AATCCACTCA CAGGGCTGCC	10560
TTTTCTCATC TTCCTGCATG GTCAACGGGG CATCTTCAAG CAAATCCACC AGATAATGAA	10620
ACTCGATATT GTGATAGGAA ACGCCGTCCA CTTCAAAACG ATTTTCAACC ACAAAGCTA	10680
GCTGCCCAGC TTGAGCTTTG ACACCCAGTT CTTCTTTCAC TTCACGGACT ACCGCGTCTT	10740
CCGTGCTTTC ATTGACTTGA ATCGCACCTC CAATAGTGTG AACTTGCCC TTGTCTTTGG	10800
TAAC TAGAAG CTGTGATT TGGACAATCA AGGCTGTAGC CCGAACACCA AAAACCGTAT	10860
TGTCTACTTT TGTCGGAAAG TCTTGTGAG TCATTCTTGT CCTTTCCCTT AAACGACACA	10920
AAAACAGTCA AAAC TACAAA GAAGTGCAGG AAAAAAAGC CTGCAACATC CAGG	10974

(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 987 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

CCCGTTATGA TTATGGATAG CGCTTTCAAA TTTTAAACT CCTATCCCAT CCTTTATCT	60
ATATAATAAG TGAAAATATA ATAAGTGTCA AGTAACTGAA GTGAATTTTA TAAAAAATT	120

1220

ACAAGCCAAA TTTGTAAAGT TTACACTAAG CCGCTAGgCA ATCGTCTATC AGAATATCCG	180
TTTATTTGTC AATAATCCGA GAAAATCTTG CAACGCTTAG AAGTCTATAA AAACATATCAA	240
CATTTATATG ACTTGCGAAT AGCAATCCTG CTAAACCTTT CCACACTCTA TCTATACAA	300
CAAGATAAAA ACATGTGTAA GCAAATCTGC TACACTTTAC TGGAGGACGC CAAGAATAAG	360
AAAAGCTACG ATAGGCTTGC TATCTGCTAT GTCCGTATTG GGATTGTGAC AGACGATTCT	420
AAACTTATCC AAAAAGGGTT CTCCCTTCTG GAGCTGACCG AGGAAACTTC TATGCTGTCT	480
CATCTCAAAA AAGAAGTAGA GACCCATTAT CAACCAAAGA AATTATAAAA AAAGTCGAGG	540
GAGCTCCTCG ACCTTTTCAT AGAATCGCCG AACGATTAA CGAGAAAGTA TGACTTTTAC	600
GTTTATCCCA ACTCAATTAT GACATTTTTT TCAAAAGTCA ATATATCTCA CTTTTTCAAC	660
GACAAGAAAG AGGCTGATAA TCTACCAACC TCTTATTCTG AACCCATCAC TCCATCACTT	720
TTTAGCTTCA TTCGCTTTCT TAGCGACTGC AATCTGGTAT TCGACTTGGT CATTCGCCCTT	780
ACCGGTACAA CCATGAGCAA TTGTAGTCGC TCCTATCTGA TGCCTATTT CAACCAATTT	840
TTTAGAAATC AGAGGGCGGC TCAAGGCAGA TACCAAGAGA TACTTTTGTT CATAATAGGC	900
ATGTGACTGA TGAGCCACTA GCACATAATC TGTAGCAAAT TCGTCCTTAA CATCAATGAC	960
ATAAGATTCT ACTGCCAAA CCTTAAG	987

## (2) INFORMATION FOR SEQ ID NO: 216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2651 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

CTGGGTCTTG TTCATAGTAG GTGTGGTtCT TTTTTTCGAG TGAGCCCAT AGCTTTGAGC	60
GCATAGTGGA TGGTAGTTGG ATGACAGCCA AAGTCAGAAG CTATTTCACT CAAATAAGCA	120
TCTGGATTGT CAGTAAGATA GTTTTAAAGT CTATCTCTAT CAACTTTTCT TGGTTTGT	180
CCTTTTACTT GGTGGTTTAG CTCTCTGTT TTCTCTTTTA GCTTTAACCA GCCATAAATG	240
GTATTACGTG AGATTGGAA AACGTGTGAT GCTTCTGTTA TACTACCTAT TCGCTCACAA	300
TAAGAGAGAA CTTTTTACG AAAATCTATT GAATATGCCA TAAGAAGATT ATACCACATT	360
GTGTACTATT TTTGGTTCAT TTTACTATAT TTTATAAGTT ATAGTGTAGC ATTCCAACCTT	420
CAAAGCACTA TAAAGTAAAT TGAAACAAGA ACAATACAAA CAATTCTCGT AAACGGATTG	480
CAACCACAAA AAAGCAAGCA TTCACAAGAA TACTTACCTA TCATGGGAGG AACAAACGTT	540

1221

CCTCTTTTTT ATTACTAAAA TTCAAAGAAT TCCAATGCTT TTTTCAAGAG CAAATCCGTA	600
TATTTCTGGAT CTTCTTGGGC TACTTCTATT TCCCGCTGAA CTTTTTCCAA ATCATCTGTA	660
ATCACTCCAT CTACTCCTAA GTGAAGAGAT TTGCTGATAG CTTCTGAATC ATTGACAGTC	720
CAGACATAAA GTTTCTGATC CGTTGTCCAT AGTTTGCTTA CAAAATATTC ATCCAAGGTT	780
GAGTACTCCA TAGTATATCC TGTGCTCTT GTTTTAGGAA AGACAGAATT GTAGGGCATG	840
ATGAAATAAA CTGGTAGTTC GGCATCATAC TGTCTTACTT TTTGACAAC ATGGTAGTCT	900
AAAGACTGGA TTTGATGTCC ATAAATCTTG AGCTTTGCAG CATAACGGGC TAAAAAGCGG	960
TTTCATCATGT CTGGACTATC TTTTTTACTG GTTTTAATTT CAATTAGTAA TTTTIGACCA	1020
AGTTCGTTGG CTCGACTGAG ATAATCTTCA AAGCTTGAAA TTTTAGTCTG GTAGCCATTT	1080
TCAAAAATAT CAATCCCTTT AAGCTCCTCC AAGTTTAAGT CTTGAGGACT TTTATTGATA	1140
CCTGCTAGAT TTTTCAAGTT AGCATCATGC ATCATGACAA ACTGCCCATC TTTTGTTC	1200
TGCACGTCGG TCTCCACCAA GTCTGGTTTG AGTTGTGCTG TAGTTTCCAA GGACTCTACT	1260
GTATTTTGAA TCCCATTTGC ATTGGAAACC CCTCGGTGAG AAATAAGTTG AGGTAGATGA	1320
ACCATGGGAG CCTCCAGATA AATATAACCT TCTAAGGCAA AGAAAAGACT GGCACAAGTC	1380
ATGACACCCC ATCGCACGAT GTGATCTTTT TCTCTCCTAG GAAGCATATC CAGCTCCTTT	1440
CCTGTCAAAA ATGAAACAAA TTTAACCAAA AAATAAGTCA GAGCCATATA ATAGAGATTT	1500
TTAATCACGA CAAAATTCAA AATACCAAGA ATCAGAGACT CTCTCTGAGT GATATCATCT	1560
ACCAAAGTTT GAGCCAATAA TAAAGGAATC AAAGGAAGAT AATAATAA ATGTGCTTTG	1620
AGCAAGATGT AAAATAAATT CCAAGCATAA AAAGTAACTC TCTTCTTGGT TTTCTCCAAG	1680
CTAAACATCA CTGCTTCTCG AACAGTCAGC TGATCATATA CAATCTTCGG AAGGGCAAAC	1740
ATCAATCTGA CAGAGACATA GAGAAAGATA AGAGATAGAA GTAGGATGCT CAGCCACCAC	1800
ATCCAATATC TATCTTCTAA ATAAGCTTGG ATAAACTCTG GAATGACGAT TTTATTAAGA	1860
TAATAAATCT TCAGCATTTT CCGTATAAAA GGAAACAGCA TAGCTATATA GAAAAGATA	1920
AACAAGGCTT TAGCGCAAGT TAGCTTTTTC ATAAATCCAA AACTTTTCATG GAAAACCTTG	1980
CGGATATACT CAATTAGCCT TCGCTTTTCA TTATAGAGGA GATGACGACC ACCAATAAAG	2040
AGGAGTCCTA TTTGAAAATA AGCAACCAGA AGGTTAATTA CAATCAAGGC TAAAAAGCT	2100
AGACTAATCA ATGGAGAATG AGTAAGGATG GCTAAGACAT TGTATAGGA AATAAAAAGA	2160
TAACCTGTCT GATCTAATAA GAAGCTAGCC AACCATGAAT TGAATGGTAC CCACAATAC	2220
TCCACTATCA TAAAAATCAA GAAAAATAGA AAGAGGATTT TATCAAGATC GAGGTAAATC	2280



1222

TGTTTAAGAC CCAATTTT	AGGTTTTTCA GGTTCATAG	GCACTCCTAG TCAAATAATT	2340
GAGACAAGTC CAAGCCACCA	AAAGGATTGT TTGATAAGCT	ACTTTCCTGTC TCTAACAAAT	2400
CCCTAGCTTG ATCCGACTCT	AAGAAGGATT CGTAAACACG	CGCCGTCATC CGAGCATCCT	2460
CTAAACTATT ATGAGACTGA	CCTTGAAATC CAAGAAATGA	GGCAACAGTT TGCAATTGTA	2520
GATTGGCAAT ACCATGTAAA	TCTGAACTCC GACGTTCAA	AGCTTCATCA TACAAATCCA	2580
CCTTGACTG TTGGCTATAG	TCTAAACCAT GCTCTGCTAA	AATAGGTAAA TCACTTTTAG	2640
CAGCATTGTA G			2651

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5638 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

CGTTATAATA AACTTGTGAA	AAAATTAACA AAGGATATCG	TTCCTTGAAA GCTATGGAGG	60
AAAATATGGC TGATAAAAA	ACTGTGACAC CAGAGGAAAA	GAAACTCCGT GCTGAAAAAC	120
ACGTAGATGA GTTGGTTCAA	AAAGCTCTAG TTGCCCTTGA	AGAAATGCGT AAATTGGATC	180
AAGAACAAGT TGACTIONATC	GTGCCAAAG CATCAGTAGC	AGCTTTGGAT GCCCACGGAG	240
AATTGGCTTT ACATGCCTTT	GAAGAAACAG GACGTGGTGT	ATTTGAAGAC AAAGCAACTA	300
AGAACTTGTT TGCTGTGAA	CACGTAGTAA ACAACATGCG	CCACACTAAG ACAGTTGGCG	360
TTATCGAAGA AGACGATGTA	ACAGGATTGA CTCTTATTGC	TGAACCAGTT GGTGTTGTTT	420
GTGGTATTAC TCCAACAACA	AACCAACAT CAACAGCAAT	CTTCAAATCA TTGATTTCAT	480
TGAAGACACG TAACCAATC	GTCTTTGCCT TCCATCCATC	AGCACAAGAA TCATCTGCTC	540
ATGCAGCTCG TATCGTCCGC	GATGCAGCTA TCGCAGCTGG	TGCTCCTGAA AACTGTGTGC	600
AATGGATTAC TCAACCATCT	ATGGAAGCAA CAAGTGCCCT	TATGAACCAC GAAGGTGTTG	660
CGACAATCCT TGCAACAGGT	GGTAATGCCA TGGTTAAGGC	GGCTTATTCA TGTGGTAAAC	720
CAGCTCTTGG GGTAGGTGCC	GGAAACGTTC CAGCTTATGT	TGAAAAATCA GCAAACATTC	780
GTCAAGCAGC ACACGATATC	GTCATGTCTA AATCATTTGA	TAACGGTATG GTCTGTGCAT	840
CTGAACAAGC AGTTATCATT	GATAAAGAAA TTTACGATGA	ATTTGTAGCA GAGTTCAAAT	900
CTTACCACAC TTACTTTGTA	AACAAAAAAG AAAAAGCTCT	TCTTGAAGAG TTCTGCTTCG	960
GCGTCAAAGC AAACAGCAA	AACGTGTGCTG GTGCAAAATT	GAACGCTGAC ATCGTTGCTA	1020

1223

AACCAGCAAC TTGGATTGCA GAACAAGCAG GATTTACAGT TCCAGAAGGA ACAAACATTTC	1080
TTGCTGCAGA ATGTAAAGAA GTTGGCGAAA ATGAGCCATT GACTCGTGAA AAATTGTCAC	1140
CAGTTATTGC AGTTTTGAAA TCTGAAAGCC GTGAAGATGG TATTACTAAG GCTCGTCAAA	1200
TGGTTGAATT TAACGGTCTT GGACACTCAG CAGCTATCCA CACAGCTGAC GAAGAATTGA	1260
CTAAAGAATT TGGTAAAGCT GTTAAAGCTA TTCGTGTTAT CTGTAACCTA CCTTCTACTT	1320
TTGGTGGTAT CGGGGACGTT TACAATGCCT TCTTGCCATC ATTGACACTT GGATGTGGTT	1380
CTTACGGACG CAACTCAGTT GGGGATAACG TTAGTGCCAT TAACCTCTTG AATATCAAAA	1440
AAGTCGGAAG ACGGAGAAAT AACATGCAAT GGATGAAACT TCCTTCAAAA ACATACTTTG	1500
AACGTGATTTC AATTCAATAC CTTCAAAAAT GTCGTGACGT TGAACGTGTC ATGATCGTTA	1560
CTGACCATGC CATGGTAGAG CTTGGTTTCC TTGATCGTAT CATCGAACAA CTGGACCTTC	1620
GTCGCAATAA GGTGTTTAC CAAATCTTTG CGGATGTAGA ACCGGATCCA GATATCACAA	1680
CTGTAACCG TGGTACTGAG ATTATGCGTG CCTTCAAACC AGATACCATC ATCGCACTCG	1740
GTGGTGGGTC TCCAATGGAT GCTGCCAAAG TAATGTGGCT CTTCTACGAG CAACCAGAAG	1800
TGGACTTCCG TGACCTTGTG CAAAAATTCA TGGATATCCG TAAACGTGCC TTCAAGTTCC	1860
CATTGCTTGG TAAGAAGACT AAATTCATCG CGATTCCAAC TACATCTGGT ACAGGATCTG	1920
AAGTAACACC ATTTGCCGTT ATCTCTGATA AAGCAAACAA CCGTAAATAC CCAATCGCTG	1980
ACTACTCATT GACACCAACT GTGGCAATCG TAGATCCTGC TTGCTATTG ACAGTTCCAG	2040
GATTGTGTC TGCTGATACT GGTATGGACG TATTGACTCA CGCGACAGAA GCATACGTAT	2100
CACAAATGGC TAGTGACTAC ACTGATGGTT TAGCACTTCA AGCCATTAAA TTGGTCTTTG	2160
AAAATCTCGA AAGCTCACTT AAGAATGCAG ACTTCCACTC ACGTGAGAAA ATGCATAACG	2220
CTTCAACAAT CGCTGGTATG GCCTTTGCCA ATGCCTTCCT AGGTATTTCT CACTCAATGG	2280
CCCATAAGAT TGGTGCGCAA TTCCACACAA TCCACGGTCG TACAAATGCT ATCTTGCTTC	2340
CATACGTTAT CCGTTACAAC GGTACACGTC CAGCTAAGAC AGCAACATGG CCTAAGTACA	2400
ACTACTACCG TGCAGATGAA AAATACCAAG ATATCGCACG CATGCTTGA CTTCCAGCTT	2460
CTACTCCAGA AGAAGGGGTT GAATCTTACG CAAAAGCTGT CTACGAACTC GGTGAACGTA	2520
TTGGGATCCA AATGAATTTT AGAGACCAAG GAATTGACGA AAAAGAATGG AAAGAACATT	2580
CTCGTAAATT AGCCTTCCTG GCTTATGAAG ACCAATGTTT ACCAGCTAAC CCACGTCTTC	2640
CAATGGTAGA CCATATGCAA GAAATCATCG AAGATGCATA CTATGGCTAC AAAGAAAGAC	2700
CAGGACGCCG TAAATAATTG TTTATCAGTC TAGAAGCAAG ACAAAAACCTC AATTTGAGGG	2760

1224

AAAGATCCAG TAATTTTCT ATGATAAAG GCATCCTATC AAGGTTTTTG AACACCTGAT	2820
AGGATGCCCTT TTTATGATAT TGAGGCCTTT TTGCCCTTTT TGAAAAACTA GAATAGAAAC	2880
AAAATATATA ATAGATTGAA ACTAGAATAG TACATATCTG CTTCTAAAC ATTGTTAGAA	2940
TTGATTTTGA CTGTCCTGAT CGATTTGTCC TGTTCCTATT TCATTTTGAT ATATAAAAAA	3000
TATAGTATAG TAGACTGAAT CTAAATAGT ACGAAACAAT TGCTAAAACA TTTATAGAAA	3060
TTAATTTTAC TTTCTGATA GAGTTGTTC CATCTTATT CAATTCACCTA TAGTTTAATT	3120
TAAGAGTAGT ATTTACTAAG GCCCAATTAA AATCAAAGAG CAAACTAGAA AACGAGTGCC	3180
ATTCAGCTCA AAACACTGAT TTGAGATTGC AGATAAGACT AGCCCCCTCA TTAACAGATT	3240
TACGATAAAA CGATGACAAG GTGTGTTGCT TTTTGATTTC TAAAGACTAT AATGATAGAT	3300
CTCTATAAAA TAAGTCCGAA GGAAATGAGC TTTTATAGTC CTTTCGTTTT AAAATACTAT	3360
CTCAGATATT CTTATATCGA CAAGAAGTTT TTGAGTCATT CCTCATCAT ACATATTAAA	3420
TAAATAGTGG CTCATTCAAT TTTTCACTAG AATAATAAGC TAGTATAGTA AACTGAAATA	3480
AGATATAAAC AAATAAATTG GAGCTTAACA TCCATTTCCA GCAATTTTTT AGAACTACA	3540
GTGGACTATT CTAGATTCAA CATATTATAA AAACCTAGAGT AAAAGAAAAG GATTGGATCT	3600
TGTGTAATGC AGGATCCAAT CCTTCAATC ATTTTGTTCCA ACTTTTGAGG GTTCCTACAA	3660
TGTAGTCGTC ATTAATAAAG ACAGATGGGA ATGACAGTGT TCCTATTTAT TTTGATAGAG	3720
ATCGATGAAT TCTTTAGATA GCAACTGAAT AATCTCTGTT GAAGCCATTT GGTCTTCTGC	3780
ATGCATAAAT AGCAAGGAGA ATCCTATTTT TTCTCCAGTA GCTTCTTTTT GTATGAGATT	3840
AGAGTGAATC TTGTGCGCTT CTACTAAGGA GTCTTCCGCT TCTTCAACTT TAATTTTCGC	3900
TTCTTTTAAA TTTCTGCCT TAGCTAGTTG GATGCTTCA ATAAAGGATG ATTTGGCTGC	3960
TCCACTATTG GCAATGAGCT GAAAACAGAT ATATTCCATT TCTTCTGTCA TCTTATTTCT	4020
CCTATCCATG CAAGTGCTTG TTCCAGAACT TTTGCTCCAT TCATCATTCG GTAATCCCGC	4080
ATATCAATGG TATCTACAGG GATATTTCTT GCAATTTCTT TCACAGCAAG TAACTCATAA	4140
CGAATTTGTG GCCCAATTAG AATGACATCT GCTTCATGGA TATTCCTTTT AGCTTCTGTC	4200
ATTGATTTTG CTGGATAGA GATTTCAATC CCACGTTTCA TCGCACTTTG TTGCATTTTT	4260
TTACAAGCA TACTTGTCGA CATTCCTGCA TTACATACTA ATAAAATTG TTTCATAATC	4320
TTAACCCTCC ATTTCTTGTT CAACAACCTT GTCATTAACT TTGATAAATG GAATGTATAG	4380
AAGAACTCCA AGTGCAAAGA TGATGAATTG AACTAGAATC GCTCTCACGT CCCCTGCTGT	4440
TGCTAACCAT GCATTTAAGA ATACTGGTGT AGTCCAAGGA ACTTGATATA ATGCAGGACT	4500
CATGAATTCT GTAACGTGTG CTAAGTAGCT GATTAAAATA CCAAGGACTG GAACTGTGAT	4560

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AAATGGAATA GCTAATGAAA TGTTATAAAC GATTGGGTAA CCGAATAATA CTGGTTCATT	4620
GATATTGAAG ATACCAGGTC CAAAAGATAA TTTAGCCACG TTTT TAGAGA CAGCATTGCG	4680
ACTCACTAAG AATGTTGCTA TTAATAAACA TAATGTAGAT CCACTACCAC CCATTAAAGC	4740
GAATGTTTGT ATTTGTGATA GGTGATGAT GTGTGGAATG GCTTGTCAT TATTGCTGC	4800
AGTGATGTTT TCAGTAATGT TAATTAATAG TAATGGTCT AGGATGGCAC TGTAAATAAC	4860
TGCTTGGTGA ATACCAAATA GCCATAACAT ATTCCTAAA GAGTAAATAA TAATGACCCC	4920
GATTAAGCTT GTACCAATAT GACGAATTGG TTCTTGAATA AAGATTGTAA TGATTGAGAT	4980
TAAGTTCATT CCAGTTATAT TGAATAATAA TGCTGAAACA ACCCCAAATA AGGAGATGAC	5040
GGTCATGACT GGAAGTAATA CGCTAAATGA TCTACTAACA GCTGGTGGAA TATTTTCACC	5100
AAGGTTTCATT TGTAAGCTT TAACGTTTGA TAATCAATG AATAATTCTG TTGCAATAAT	5160
CGTACGATAA CCCCGGCGAA CATTGCGCCT GTACCTGTGT TGTGAATGA AAGAACACCT	5220
GAAATGTTTA CCGCATCTTT TGCTCCGTCA GGAAC TACAG AAAGTGTATT TGGCATCATC	5280
ACAATTAAG AACTAATGA TAGCATTGAT GCTGCTAACG GGTTTTCGAA ATCTCTGTTT	5340
TTAGCTAAGA AATAACCAAC CATTACAGCA ATAATCATAC CTGAAATACT TAAAGTACCG	5400
TTTGCAATTG TTATTCCTCA ATATTGGAAT CTGTGTAATG TATCCCCTTG GAAATCCAC	5460
TTAAATACCG TGTTGTTCAA AAGAACGATT AAACCTGCCA AAATATATAA TGGCATTACT	5520
GTTACGAATG CATCTCTTAG GGTTTTTTAA TGAATTGGT TCCCTAGTTT ACCAGCAAAG	5580
GATGGCAAAA AAATTTTTTT GGGGGGGGG GTTATTAAAC CCCCTTTTTT AAAAAAAA	5638

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4745 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

CCGGAAGCTG TTGCCCTTGG AACTCCAAAT GAAGAAACAG CCTTGTCTT GAACTATTTT	60
GGTGTGGAAG CACCACGTGT TATCACTTCT GCCAAAGCAG AGGGGGCAGA GCAAGTTATC	120
TTGACTGACC ACAATGAATT CCAACAATCT GTATCAGATA TCGCTGAAGT AGAAGTTTAC	180
GGTGTGTAG ACCACCACCG TGTGGCTAAC TTTGAACTG CAAGCCCACT TTACATGCGT	240
TTGGAGCCAG TTGGATCAGC GTCTTCAATC GTTTACCGTA TGTCAAAGA ACATGGTGTA	300

1226

GCTGTGCCIA AAGAGATTGC AGGTTTGATG CTTTCAGGTT TGATTTCAGA TACCCCTTCTT	360
TTGAAATCAC CAACAACACA CCCAACAGAT AAAATCATTG CTCCTGAATT GGCTGAATTG	420
GCTGGTGTGA ACTTGAAGA ATATGGTTTG GCAATGTTGA AAGCTGGTAC CAACTTGGCT	480
AGCAAATCTG CTGAAGAATT GATTGATATC GATGCTAAGA CTTTGAACCT CAACGGAAAT	540
AATGTCCGIG TTGCCCAAGT GAACACAGTT GACATCGCTG AAGTTTGGGA ACGCCAAGCA	600
GAAATTGAAG CTGCAATGCA AGCTGCCAAC GAATCAAACG GCTACTCTGA CTTTGTCTTG	660
ATGATTACAG ATATCGTCAA CTCAACTCA GAAATCTTGG CTCTTGGTGC CAATATGGAC	720
AAGGTCGAAG CGGCTTTCAA CTTCAAACCTT GAAAACAATC ATGCCCTTCCT TGCTGGTGCC	780
GTTTCACGTA AGAAACAAGT GGTACCTCAA TTGACTGAAA GCTTTAATGC GTAAGATTTT	840
GGGTGTCAGC TCAAAATCGG AAAGTCTAGT TTGCCTTATA TCGCAAGGAG TTTCGGCTCC	900
TTTTTTCTAG GAGTGAAGTA TGTTAGAAAA TGGCGATTG ATTTTGTGA GAGATGGGTC	960
AGACATGGGA CAGGCCATCC AGACTTCCAC AGGTAACATAT AGCCATGTTG CCATTTATTT	1020
GGATGGGATG ATTTATCATG CTAGTGGACA GGCTGGTCTT GTCTGTCAAG AACCGGCAGA	1080
CTTCTTTGAG TCCAATCATT TATACGACCT CTATGTTTAC CCAGAAATGG ATATCCAGTC	1140
GGTGAAGGAA AGAGCTTGCA AACATCTTGG AGCACCTAC AATGCTTCTT TCTATCCAGA	1200
TGCAGCTGGT TTTTACTGCT CCCAGTATAT AGCAGAAATC CTACCTATTT TTGAACTAT	1260
TCCTATGAAA TTTGGAGWTG GGGAGCAGGA GATTAGTGAT TTTTGGAGGG AGTATTACAT	1320
AGAACTAGGT CTGCCTGTTC CTCTGAACCA AGCTGGTACC AATCCTAGTC AGTTGGCAGC	1380
ATCGCCTCTG TTACAATGTA AAGAAAGGAA TCTTCATGAT TCAGATTTT AATCCATCTC	1440
GTTTGACGAG ACAGCCATTT TTGGAGAATT GATCCGCTAT CTGGATCAGT ATGAGGATGT	1500
GATTCTACGG GAAATTAAG CTCAATTTCC AGATGTTGCA GTTGATAAAC TCATGGAAGA	1560
GTATATAAAG GCAGGCTTGA TTCTACGTGA AAATAAGCGC TATTACCTCA ATTTTCCTAC	1620
GCTTGAATCA CTTGATAGTC TTGAACTGGA TCAAGAGATT TTTGTCAGAG AAGCTAGTCC	1680
GGTCTATCAA GCCTTGTTGG AGCAGAGTTT TGAGACGGAA TTGCGCAATC AAATCAATGC	1740
AGCTATTTTA GTTGAAAAGA CGGACTTTGC GCGCATTAAT ATGACCCTGT CCAATTATTT	1800
TTACAAGGTC AAACAGCAGT ATCCTTTGAC AGAAAAACAG CAGGAGCTCT ATGACATTTT	1860
AGGAGATGTT AATCCTGAGT ATGCCCTCAA GTATATGACG GCTTTTTTGT TGAAATTTCT	1920
CAAAAAAGAC CAGCTTATGC AGAAATGCCG TGATATCTTT GTGGACAGTT AGGTTGTCTT	1980
AGGCTATATT GTGCAAAATG AAGATGGAAA GTATGAGTTG GCTATCGATT TTGATAAGGA	2040
GAGGTAACT TTCTACTTAG CGTGATTTCT TGTTTCTGAG TACATTGTTT GACTTTCCTT	2100

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AGTATTCGGT ATAAACTATA TGTAACCGGT AACACATATC GGAATAAACT AAAGGAGACA	2160
ATCATATGTC ACTTGAAAAC AAATTGGAAC AAGCAACAGG CGCTGTCAAA GAAGGTTTTG	2220
GTAAAGTTAC TGGAGACAGC AAGACAGAAC TTGAAGGAGC TGTGAAAAA ACAGTTGCTA	2280
AGGCAAAAGA CGTTGTAGAA GACGCAAAAG GTGCTGTAGA AGGTGCCGT GAAGGTTGA	2340
AAAACGTTTT TACTAAAGAA TAGGAAAAA TCAAGGGTTT CATTTTCCCT TGATTTTTC	2400
TATTCCTATA AATAATTTTC TGCGACGGCT GTATCTCCTG GGTAGGATTC TTTCTTGCCC	2460
TGGATGATTT GGTAACAATC GGCTCCCTTA CCCGCAATAA TAACTGCATC TAATTCGTGA	2520
TTTGTGATAG CCATTGCCGC CTGTATGGCT TCTGGCGAT CCGCAATCTT TTCAACAGGA	2580
TGATTGATGT AGCTACTAAT TTCATCTGCA ATGGCCATG GGTCTTCATA GTTAGGGTCA	2640
TCAGCAGTCA GAAAGACTTG AATCTCAGGG TGTGATTGA GGAGGAGGCC AAAGTCCTTA	2700
CGACGACTTT CTCCCTGTG TCTGTGTGAT CCCAGAACCA GAGCAATCTT TCCGGTTTGA	2760
TGAGTTTCAA CCACATTGAT GAGTTTTTTC AGACTATCCC CATTGTGGGC ATAGTCGATG	2820
AAGACCTGG CTCCATTTTT CTGAGTGAGG ACTTCCATAC GACCAGGAAC GCGGGTTGCA	2880
GCGATGCCTT TTTTGATGTC CTCAAGACTT GCTCCGAGAC GGAGACAAGC AAGTCCAGCA	2940
GCAACTGCAT TTTCTTGGTT GAAGTTGCCA ATGAGTTGAA TATCATAATC TCCAGCGAGT	3000
TTACCCGTAG CTGAAAAGCT AAAGGCTTTG GAATTCCTGA TTTGGTTATC AAATTGGCTA	3060
CCATAGAAAT CATGGTCTTG ATCTTCAACC TGTTCCTTCA AGACTGAGAA GTGGTCCATG	3120
TCACTGTAA TGATGACTGC TCGGCTCTTT TCCATCAAGA GACGCTGTG GTAGAAATAG	3180
TCTTCAAAGC TAGGGTGTTT AATCGGGCCG ATATGGTCTG GGCTGATATT TAGGAAAAC	3240
CCCACATCAA AGGTTAGACC ATAGACACGT TTGACCAGAT AGGCTTGACT GGAGACTTCC	3300
ATGATGAGGT GGGTACGGTC ATTTTGCACA GCCTGATTCA TCATGTCAAA GAGGTCAATA	3360
CTCTCAGGGG TTGTCAACGC TGACTTAAAG AAAGTCTCGC CATCAAGAGT TGTGTTTATG	3420
GTCGACAACA TAGCAGGTCT ATGCCCTTGA GATAAGATGT TATAGGCGAA ATAGGCTGCT	3480
GTTGTCTTAC CCTTAGTACC AGTAAAGGCA AGGAGTTTGA GTTTTTCCTG TGGATTACCA	3540
TAGAAGTCCA TGGCAATCAA ACTCATGGCT TTCTTTATAT CGTTCACAAT GATGACAGGG	3600
ATACCGACTT CGTAGTCCTT TTCAGCTACA TACCAAGCTA ATCCTTGTGT TATAGCAGAA	3660
AGAAGGTATT CTTTTTTAAA GGCAGCGCCT TTTGCGAAAA AAAGAGTGTC TTCTGTACT	3720
TTTCGGCTGT CGTAGCTGAT GCTATCAAAA ATAAGTTGC TGTAGTTGTA GTGGTAATGA	3780
CCTTGGTCAA TAATTCGCG AAAAAGGCCA TCTTCTTTA AAATATCTAA TACGCTTTCA	3840

1228

ATCTTAATCA TACTTTCTAT TGTAACCGA AAGTCGTAAA TTTACAAGTA ACAAGGAAAA	3900
GTTTATAATG GAAGATAAGG AGTTTTTCCT AGTTATCAAA ATTGAATGAG GAATCTATGT	3960
CGCACGAAAA CAATCACCAG CAGGCCCAGA TGTACGGGG GACTGCTTGG CTAACGGCTA	4020
GTAACCTTAT CAGTCGCCTA CTCGGGGCTG TTTACATTAT CCCTTGGTAC ATCTGGATGG	4080
GGGCTTATGC AGCTAAGGCA AATGGTCTCT TTACCATGGG TTACAATATC TATGCTTGGT	4140
TCTTGTTGGT TTCAACAGCG GGGATTCCAG TTGCGGTGGC CAAGCAAGTT GCCAAGTATA	4200
ATACCATGCG AGAAGAAGAG CATAGCTTTG CCCTGATTCG GAGCTTCTTA GGCTTTATGA	4260
CAGGACTAGG CCTGGTTTTT GCTTTAGTCT TGTATGTCTT TGCTCCTTGG CTAGCAGACT	4320
TGTCCTGGCGT GGGCAAAGAC TTGATCCCAA TCATGCAAAG CTTGGCTTGG GGAGTCTTGA	4380
TTTTCCCGTC TATGAGTGTT ATCCGAGGAT TTTTCCAAGG GATGAATAAC CTCAAACCCCT	4440
ATGCCATGAG CCAAATTGCT GAGCAGGTCA TTCGTGTTAT CTGGATGCTC CTAGCAACCT	4500
TTATCATTAT GAAGCTCGGT TCAGGAGATT ATCTAGCAGC CGTTACCCAA TCAACCTTTG	4560
CTGCCTTTGT CGGTATGGTA GCCAGTTTGT CAGTCTTGAT TTATTTCTT GCGCAAGAAG	4620
GTTCACTCAA AAGAACTCTT GAAACAGGAG ATAAGATTAA CAGTAAGCGT CTCTTGTTG	4680
ATACCATPAA GGAAGCCATT CCTTTTATCC TGACAGGGTC TGCCATCCAG CTCTTCCAGA	4740
TTTTG	4745

## (2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1900 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

CCTGATTGAC CTTATAATAA GGAACAAAAC ACAATGCACT ACCTTTTCAA CAAAAGAGTT	60
GCTGCTTGAT TAAAACCATC ACACCAGTTA TACCATTTTG CTTTATACCC ATCTTGAGCT	120
AGGATACCAT CTTCTAAATC AAAACAGAG TAAATCTTTC TTTCTCGCA AGCTTGCGCA	180
TAGAGATGAT ATAGTTCATC ACCACCATCT CTATCCCACT CAGCAGAAAT CGTATCCCGA	240
CCTGCCAATA AAGCCTGATA AGCCCTGTGA TGCCCATCTG TAATCAGCAA ACAATCTCCA	300
AAGGCAAGAA TACTGATTGG ATCGACTTGG ATTGTTTCTG CCGACTGGTA AAGCATCTGA	360
ATATCTTGCA ACTTCTTTTC TGATAAATAT AGTTGAGTCA GATGAAGATC TGCTATATTG	420
ACTTTCATTT CTTTCTCCTC AAGGGAATTC GATACTCACT TCTGTTTGCC TTTAAATCGC	480

1229

CATTGGAAGC GGAGCTTGTC ATAAAAGGGA AACTCGATAA ACAGGACTCC CAAGCCCACA	540
CAGAGACTGG CAAGGACGTC TGATGGGTAA TGAACGCCA GATAGACTCT TGATACCAGC	600
ACACTGACTA GGTAGAGGCC AAGGACGATT TGTACGATTT TTCTCCAGAC CTGATCTTTA	660
ATCCGCTGAC TAAGAATAAC AATCAAAGTC CCTACCATCA GCGTTACAGC TAGAGAATGC	720
CCACTTGGGA AGGAAAATCC CTTCTCCTCC ACCAGATGTA AAATAGCTGG TCGTGGGCGC	780
TGGTAGATAT TTTTAAAGGT CACGATTAAA AGACCTGCCA AAGCCAGATT TCCCAGCATG	840
AAGAACTTT CTATCTTCCA TCGCTTACGA TAAAAGACAA AAGCTGTAAT GACAACCCAA	900
GTGATAATCA CTGGGATATC AATCAGACGT GTGAGGGCTC GAAAAAGAAT AGTCAAATAA	960
TCTGGTAACT CTCCPCGAAT GGCAGTCTGA ATCGATTGGT CAAAATTGAC CAACATTTCA	1020
GGGTAAATTT TGACCATGTA GCCAAGAATA ACGAAAAGTA AAAGGGCAAA ACTGCCCTTC	1080
ATTAAAAATG TTTGTATTATC TCTCATAATG TTTTAAGGTT GGTTCAGA GAACATACAA	1140
CAACCAGAAAT GAAACGGAAA AGATAACACC TTCATCAAG TTAAGGTA ATACCATGGT	1200
CATTAGGTAG TTGGAAAGTC CCAAAATTTT TCCAATATCA AAGTTAGCAA ACTTAGCGTA	1260
CAAAGGAACA GCATAAACAT AGTTGAGAAC CAACATGGCC AAGGTTAAAC CAATAGTTCC	1320
AGCTAGAGAG CCTAGTAGGA AACGAAGGT TGTCCGTTCC TTTTCCAAA TCAAAGCAAA	1380
TACGATGACA AAAACTCCCA AAGCTACGAT ATTTCATCGG AAACCAATGT AAGTATTCAC	1440
TCCTTGGCTG TTAAGAAGCA ATTTCAAGAG TGAGCGAAGC AAGAGCACTC CTAGAGmCsC	1500
AGGCAAATCC ATGACCACCA GACCCACAAG GACTGGCAAG ATACTAAATT CGATCTTGAG	1560
GAAAGATGCC GCTGGTAAAA GCGGAAAGTC AAAGTACATC AGCACAAATG AGATGGCTGA	1620
TAGAATTGCA ATGGTCGAAA GTCGACGIGT GTTTGTCATA ACAGGTTCCCT CCAATTTTCT	1680
ATAAAATCAG AAGAAGTTGG AAAGGATICC TCTATCTATT CTCACTTTT ATATCCCAA	1740
AGTTCCTCT TACTCTATTA AAGAAAAACA AAGCAAGTGG TTACAATCCG GCTATAAATC	1800
TATCAAACA GACAAGGCTA TTCTTTCGTC TTCTCCCATC CAGACTATAC TGTCGGTTGT	1860
GGAATCTCAC CACATCACGT TGCGCTCACG GACTTCTTTA	1900

(2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4692 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



1230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

GGTTTTCCAG CAGGAGCTTC TCCTTTATCA GAATGACCAT CCCATCTGCT CACGATAGAT	60
GAATAATGAT ATTTTTTACC ATGATAGTAA TTTGAAAAAG CCTAACCACC TCCTGAACCT	120
TCTCCATATG TCCATACTCC TCCATCTGGA TATTATACAG CAGCTGATGC AGCTCCCAAT	180
AATGTAAAC TTGAAATAAG AGCTAGAGCA AGTAATCTAT GTTTTTTCGT TTTCATTTTA	240
TTTTTCTTT CAAAAAAGC ACACCTTGAG CAACAATGCA ACAAATAAA TCCTCCTCTC	300
TCTTTTATG AAACCGCTTT CTATGTGAT AAGAATAACT TTTTATtAT TTGTGTCAA	360
GGAAAAATC GAATTTTTTA GATATTTTAC TATATTACCT CTGTGAATAA TATTATATAG	420
TAGTTTTATT TCAAAATAAT ATGCAACCAG TACTAACCAA ATATAAAATA GATGCCATTA	480
ACGAATTTTA TTCAAGTTTT TCCCATTCAT ACTATACAAG TAAAAGAGAT GGTGTAACT	540
AAAAAGCAAT TCAAACTATT GTAAAATTC TAGCAAAAAG AGAGCCGAAA CTCTCTTTTT	600
TATCTTCTTT TACTTTTTTT GACTGGCATG AGTGTGATGT CTCTAACACT AAAGTAAGCT	660
AGGATCAACA TGGCTATTGC TAGGAATATT TCTGTTGGTA ATTGAAAAAT TTTCAGAAAA	720
GATAGAACCA ATAAATCAA GAGTGCCACT AAAATACATA CCATAGCGAC GATATTGACA	780
GTCCCTTTAA TGCTTCTGG TGTGCGAAAT ACATAGAGTA GGAGCAGTAA AATTCCTAGG	840
ACTAAATAGA CCATCTTCT CTCTTCTAG CTCTATTCA GCTGATTTT TCTTCTTGTT	900
AGCTTCTCTA CGCTCTGCTT TGTTAAGGAT TTGTTTACGC AAACGATAG ACTCAGGCGT	960
TACTTCCATG TACTCATCGT CGTTCAAGAA CTCAAGAGAC TCTTCAAGTG TCAAGATACG	1020
AGGCGTCTTG ATAACAGCTG TTTGGTCCCT AGTAGCTGAA CGAACGTTGG TCATTTGTTT	1080
TGCTTCGTG ATGTTAACTG TCAAGTCATT TTCACGAGAG TTTTCACCGA TGATCATTCC	1140
TTCATAAACC TCAGTACCTG GGTGACAAA GATCGTACCA CGTTCTTCGA TAGACATGAT	1200
TGAGTAAGTT GTAGCCTTAC CAGCATCGAT AGAAACAAGG GCACCACGGT GACGTCCACC	1260
AATTTCCCTT GGAATCAATG GCAAGTATTG GTCGAAGGTA TGGTTCATGA TACCGTAACC	1320
ACGAGTCATT GATAAGAACT CAGTTGAGTA TCCAATCAAA CCACGCGCTG GAACAAGGAA	1380
GACCAAACGA GTTTGACCAT TACCAGTTGA AATCATATCC AACATTTTAC CTTTACGTTT	1440
AGAAAGGCTT TGGATAACAG ACCCTTGGTA TTCTTCTGGA GTGTCGATTT GTACACGTTT	1500
AAATGGTTCA CATTTAATAC CGTCGATTTT TTTTACGATA ACTTCTGGAC GAGATACTTG	1560
AAGTTCATAG CCCTCACGAC GCATTGTTTC GATAAGGATT GACAAGTGCA ATTCTCCACG	1620
TCCTGAAACA GTCCATTTAT CTGGTGAATC AGTTGGGTCA ACACGAAGGG AAACGTCTGT	1680
TTGCAATTCT GCCTGCAAGC GTTCTTCCAC CTTACGAGAA GTTACCCATT TACCTTCTTT	1740

1231

ACCAGCAAAT GGTGAGTTGT TGACCAAGAA AGTCATTTGA AGAGTTGGCT CATCGATGTG	1800
TAGGATTGGA AGAGCTTCTA CTGCATCTGT CGGAGTGATG GTTTCACCGA CAAAGATGTC	1860
TTCCATACCT GAAACGGCAA TCAAGTCACC CGCTTTGGCT TCTTGGATT T CACGACGTTT	1920
CAAACCAAAG AAACCGAAGA GTTTTGTAAC ACGGAAGTTT TTAGTTGTAC CGTCAAGTTT	1980
AGAAAGGGTA ACTTGGTCCC CAACCTTAAC TGTACCACGG AAGACACGAC CGATACCGAT	2040
ACGTCCAACG AAGTCATTGT AGTCCAAAAG TGACACTTGG AACTGCAAAG GTCATCTGA	2100
GTTATCTACT GGAGCTGGGA TATGGTCGAT AATCGTGTC AAGATTGGTG CCATAGTCGC	2160
TTCTTGGTCA GCTGGATCAT CTGACAATGA AGAAGTTCCG TTGATCGCTG AAGCATAAAC	2220
CACTGGGAAA TCAAGCTGGT CGTCATCTGC ACCAAGCTCG ATGAAAAGTT CCAAGACTTC	2280
ATCCACTACT TCTGCTGGAC GAGCTGATGG CTTATCGATT TTGTTAACA CCACGATTGG	2340
GACAAGGTCT TGTTCGAAG CTTTTTTCAA TACGAAACGA GTTTGTGGCA TGGTTCCTTC	2400
ATAGGCATCT ACGACCAAGA CAACACCGTC AACCATTTTC ATGATACGCT CAACTTCTCC	2460
ACCAAAGTCC GCGTGTCCG GTGTGTCCAT AATGTTGATA CGAGTTCCGT TGTAAGCAAC	2520
GGCAGTATTT TTAGCAAGGA TGGAATTCC ACGCTCTTTT TCGATATCGT TTGAGTCCAT	2580
AGCAGCTCT GCCAATTCAG TCCGTGCATC AAGCGTTTCT GATTGTTTCA ATAATTCTCT	2640
AACCAGGGTT GTTTTACCGT GGTCAACGTG GGCATAATC GCAATGTAC GGATATCTTC	2700
TCTTAATTTT GTCATGATTT CCTCTATAAT ATTCAAATT TATTTCTCAA CTGAACGATT	2760
ATACCATAAT TTCAAATAA TAACATAACT CAAGCAAGTG TAAATGTTTT CACTCTGCTT	2820
TTCTTTTCAC GTCAAGCCTT TTCAAAGCGA GCGACTTATG ATAAGATAGG CACAGTATGC	2880
GTTTAGATAA TTTATTAGCT CAAGAAAAA TCAGCCGAAA GGCCATGAAG CAAGCACTCC	2940
TCAGAGGGGA AATTCTAGTC GATGGTTGCC CAGCCCGCTC CCTAGCTCAA AATATCGATA	3000
CAGGACTACA AGAACTCCTT TTTCAGGATC GAATCATTCA AGGCTATGAA CACACCTATC	3060
TTATGCTTCA TAAACCTGCT GGTGCCGTTA CAGCCAACAA AGACAAGGAA CTCCGACCG	3120
TCATGGACCT GCTTCCATCT AACATCCAGT CTGACAAGCT CTATGCCGTT GGCCGACTGG	3180
ACCGAGATAC AACGGGACTC CTCCTCTTGA CCGATAACGG TCCCTTGGGC TTTCAGCTCC	3240
TCCATCCCCA ATATCATGTC GATAAGACTT ACCAAGTTGA GGTAAATGGA CTTCTAACAC	3300
CTGACCATAT CCAAACCTTT CAAAAAGGAA TTGTCTTTTT AGATGACACT GTCTGTAAAC	3360
CCGCAAAACT AGAGATTCTA TCTGCAAGTC SCTCCCTCAG TCAAGCCTCT ATCACCATTT	3420
CAGAAGGAAA ATTTTCATCAA ATCAAGAAAA TGTTCCTCTC GGTGGTGTT AAGGTGACTA	3480

1232

GCCTCAAAAG AATCCAATTT GGGGACTTCA CATTTGAACCC AGATTTAGCA GAAGGTAAC	3540
ACCGCCCTTT GAACCAAAAA GAGTTACAAA TCATTAAAA CTATTTAGAG ATGAGTCGAT	3600
AAAACAAAA AAGCTTTAAA ACTAAAGCTT TTTTCTTTTA TTTACCGAAA AATTAAGGCG	3660
ATTGCTACAA TCCAGTTAAC TACAGAAATC ACAATTCCTA AGATATTAAG AATCTTTTCT	3720
ATTTTATAGT CTAATTGTGA CTCTTTTGG TATGAAATAG CCAAGACCAA TCCTATGATA	3780
CCCAAAATCA GGCCTACAAT TGGAAATAAC AAACCAAGAA TAATCGACAA GATACCCACA	3840
AAAAGTGGAT TTTTCTTCTT TTCTTTTATG TTCTAAGAAC TCCTTAAATT TTATACAAAT	3900
TAATTATACT ATAAACAAT AGCTTCATCC TATCATTCGA CTAATTGGA AATAAGGTTA	3960
GCTAGTCTTC ACTTTCCTT TCCAAGAATC CAAGCCATAA GAAAGGATAT AAATCTCAGA	4020
AAAACCTTGT TTTTCAAGT AAAGAGCTGC ATTTGTAAC CGTTGCGCAC GTTGGTTTTC	4080
GTAGAGAAGG ACAGGTTTAT CTTTACGAAG GGCTGCAAGA CTACTTTTCA ACTGACTTGA	4140
AGGAATATTG CGTGACCAA GGATATGTTT TCTGTGGAAT TCTGCTGGT CGCGCAAATC	4200
AATCAATGA CCCGTACGAA TCAAGGCTTC AACTCCTCA TTGTCCACAA TTTTAGCCGC	4260
ACGGCGAATA CGAAGATAGT TAAAGCCCAT CCACGCCAAC ATTGCTAGTA TAAGTGCCCA	4320
CAAAATCCAA GTAACCATTA GTTCTTTTCT CCATTTTCT CAATATAATC CAATTCTACC	4380
TTGTGCTCTC TGCGAAGAAC TGCTTCTGCC TCTAGATAGT CTAATTTATC CATCAACCTT	4440
GCATCGTAAA TCCGAGATAG TTCCAACCTC ATCAGTTCAA TATCATATAA GCGTTTTCCT	4500
ATGTAAACAA TAATACCAA TCGTTTGAGG AATTGCTGCA CATCATAGAA TGTTTTCATA	4560
AGACTCATTC TAGCAAAAT TTGTGTTTTT TTCAAGAAGA GACTCACACA ATGCTCCTTA	4620
TTTTCCTATC TTCTTTAGCG ATTCTAAGGC AAGTATGGTA CAATAAAAAC ATGGGGATTC	4680
AACAATTACA TT	4692

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 706 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

GCTAAAAAGC TGATAATCTT CGACTCCTGT ATATGATGTG TCTTTTCATG TAAGACACGC	60
GCCGCCAGAA TCATGGCAAG AGCTGCAAGA CTGGCAAGTA AGAAGCCGAT AAGATAGGCA	120
AAAAGATAAG TGAATTTGAC AAAGAAAGTC AAAAGAACTA GGAAACCAAA GCCTCCTCCA	180

1233

AAAAC TACCA AAGTCTTTCG TAAATCCCAG ATTTTATCCA ACTGCTTGAC GAGGGAAGTC	240
GTCTGACGAA CGCCTACAAT AGTTGCTAAC ATACTTCCTA AAAAGAATGG ATAGACATGA	300
GTTAAACTGG AGAAATAAAC AGAGGAATAA GAGGTCAC TA GAAACTACC AATAAACATG	360
GAGAAGAAAC TGATCAAGAA GGCAACAGCA GATAAGAGAA AGACCATCCC CTTC AACTGA	420
CCATTGATT TAGCTTGTTT GGATAAGAAC CAAACTGCCA ATCCCCAAG AATATAGTAG	480
TGAACCTCAA CTGCCAAACT CCAATTATGA ACAAACAAAT GAGGAATGAA CTGAGATTCA	540
TAACTCCAC CTGTTAGGAG TTCATAGAAG TTGGTCATAA AGCCTAAGAC GCCCGCAATC	600
TGGCCACCAA TTCCAGCAAC ATAGTCTTGG CGAACCAAGA AAGTAAAAGG CATGGTCACC	660
AAGACCATCA AAACCACAGG TGGCACAATC TCGATAAAAG CGTCTT	706

(2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3236 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CAGCTGATGG GCAATATCAG TCATAGAAAT TTTTCAATT AACTTTTGAG CAATTTTTG	60
GTTGATGATA CGAGGGATTT GGTGATTTT CTTTACCAGG GGAGTCTCAG CAACCATCAT	120
TTTTGAACAG TGATAGCACT TGAACGGCG TTTTCTAAGG AGAATTCTAG AAGGCATACC	180
AGTTGTTTCG AGGTAAGGGA TCTTAGACGG TTTTGAAAG TCATATTTCT TCATTAGACT	240
TCCACAATCA GGGCAAGATG GAGCCTCATA ATCCAGCTTA GCGATAATTT CTTTGTGGGT	300
ATCCATATTG ATGATATCTA GAATCTTGAT GTTTGGGTCT TTAATATCGA GCAGTTTGT	360
GATAAAATGT AATTGTTCCA TATGATTTT TCTAATGAGT TGTTTTGTCG CTTTTCATTA	420
TAGGTCAATG GGGACTTTT TTCTACACAA AAATAAGCTC CATAATATCC ATAGGGGATT	480
TACCCACTAC AAATATTATA GAGCCCGAAA ATATGGGAAA ACTGATCCTT GTTTCTGCTT	540
TTGTCTATAG AAGAATAATA AAGATTATCT TCTTCAAAT CTCCGATATT CTCTAAAGTT	600
TTGTGCAAGT TGCACAGAAC TTGTTTATTT TTTTGGTCAT CTTGCCATAG AAATATAAAG	660
CGTTTTCATA TATAATATAA TTATCAAAAG ACAAAGGAG TTCACCTCAT GGTAGAATTG	720
AATCTTAAAA ATATTTACAA AAAATATCCA AACAGCGAAC ACTATTCAGT TGAAGATTTT	780
AACTTGAACA TCAAAGATAA AGAATTATC GTTTTCGTAG GACCTTCAGG ATGTGGTAAA	840

1234

TCAACTACAC	TCCGTATGAT	TGCTGGTCTT	GAAGACATTA	CAGAAGGTAC	TGCATCTATC	900
GATGGCGTAG	TTGTCAACGA	CGTAGCTCCA	AAAGACCGTG	ATATCGCCAT	GGTATTCCAA	960
AACTACGCTC	TTTACCCACA	CATGACTGTT	TATGACAACA	TGGCTTTCGG	TTTGAAATTG	1020
CGTAAATACA	GCAAAGAAGA	CATTAACAAA	CGTGTTCAAG	AAGCAGCTGA	AATACTTGGA	1080
TTGAAAGAAT	TCTTGAACG	TAAACCAGCT	GACCTTTCAG	GTGGTCAACG	TCAACGTGTT	1140
GCCATGGGGC	GTGCGATTGT	CCGTGATGCG	AAAGTATTCT	TGATGGACGA	ACCTTTGTCA	1200
AACTTGGATG	CCAAACTTCG	TGTATCAATG	CGTGCTGAAA	TCGCTAAAAT	TCACCGTCGT	1260
ATCGGAGCTA	CAACTATCTA	TGTAACCTAC	GACCAAACAG	AAGCGATGAC	ACTTGCAGAC	1320
CGTATCGTTA	TTATGTCAGC	TACTAAGAAC	CCTGCTGGTA	CAGGTACTAT	CGACCGTGTA	1380
GAACAAATCG	GTACTCCTCA	AGAAGTTTAC	AAAAATCCAG	TTAACAAATT	CGTTGCAGGA	1440
TTCATCGGAA	GCCCAGCTAT	GAACCTCATC	ACCGTGAAAT	TGGTTGGTAG	CGAAATTGTT	1500
TCTGACGGTT	TCCGTTTGAA	AGTGCCAGAA	GGAGCATTGA	AAGTTCTTCG	TGAAAAAGGC	1560
TACGAAGGAA	AAGAATTGAT	CTTTGGTATC	CGTCCAGAAG	ACGTGAATGC	AGAACCTGCT	1620
TTCTTGAAA	CATTCCAGCA	CTGTGTTGTA	AAAGCGACTA	TCTCTGTAIC	AGAACTGCTT	1680
GGTTCAGAAT	CTCACCTTTA	CTGTCAAGTT	GGTAAAGACG	AGTTTGTTCG	AAAAGTTGAT	1740
GCTCGTGACT	ACTTGCAAAC	AGGTGCAACA	GTTGAGCTTG	GATTTGACTT	GAACAAAGCA	1800
CACTTCTTCG	ATGTAGAAAC	TGAAAAAACA	ATCTACTAAA	ATAAATAAAA	TTCAAAGCAC	1860
TACAAGAAAA	GATATCTCTT	TATCAATTGT	AGTGGAGAGA	TATCAGTTAA	TCTAGGGAGA	1920
GAAACAAAAAT	GCTTCTCTCC	TTTTTGCTAG	AGAAGTCATA	TTATGCATCT	ATATTGTGAT	1980
GCTCTTTAAT	ACTCTTCGAA	AATCTCTTCA	AACCACGTCA	ACGTCGCCTT	GCCGTACGTA	2040
TGATTACTGA	TTTCGTCAGT	TTTATCTGCA	ACCTCAAAGA	TGTACTTTGA	GCAGCTTACG	2100
GCTAGTTTCC	TAGTTTGCTC	TTTGATTTC	ATTGAGTATT	ATTTGTGGGT	ACCATCTACA	2160
AGTGAAGCTA	TATGCGTAAA	CTACGTGAGC	AATTGAATTC	GAAGTAGAGA	GGTAATAATA	2220
AATTTATGCT	ATAGTTATGG	TGACTTGAT	GCTTTTGATT	CTAGTTTATC	AAATAATAGA	2280
TTAGAATTGT	CAGATAATAT	CATTTTGTGT	TATAATGAAG	AAAAAACAGA	GGTGTTCAAA	2340
TGTCAGAAAGC	AGGTCATAAG	TTTTTAGCAA	AATTGGGGAA	AAAACGCTTA	CGTCCAGGTG	2400
GAAAGCGTGC	CACAGATTGG	TTAATTGCAG	AAGGAGGATT	TTCAAAAGAA	AAGAGAATAC	2460
TAGAGGTTGC	GTGTAATAGG	GGAACACAG	CAATTGAGTT	GGCACAGCGT	TTTGTTTGCA	2520
AGATAACTGC	TGTTGATATG	GATGCTCAAG	CTTTAGAAGT	GGCTAAAAAA	TCTGCTGGAA	2580
CGGCAGGTGT	TGCTCATTTA	ATCAGTTTGT	AAAGAGCAAA	TGCAATGAAA	CTTCCTTATC	2640

1235

AAGATGCTAG TTTTGATATT GTTATAAATG AAGCTATGCT GACTATGCAA GCCGATCAAG	2700
CTAAGAAAAA ATGTGTAATG GAATATCTAA CCGTATTAAA ACCTGGAGGT CTTCTCTTGA	2760
CACATGATGT GCTTCTTAAG GAAGCTAAAG AGTCTATCAG ACAGGAATTA TCACAAGCAA	2820
TTCATGTAAA TGTAGGTCCT TTAAGTCAAG ATGGTTGGGA ACAGGTGATG ATAGAATCAG	2880
GTTATTGTGA TGTGAAAGCA TTGACTGGTG AAATGACATT AATGAAATTA TCGGGTATGA	2940
TTTATGACGA AGGTTTGCTA GGAACCTTGA AAATTTGTGT AAATGCTTGT AAAAAGGAGA	3000
ATAGAAAGCA GTTTTAACT ATGTATAAAA TGTTTGCTAA GAATAACAG AAATGGGCT	3060
TTATGCGAT GGCTAGTTAT AAATCGTCAA AACGTTAGAT AATTATTGAA GTTAACTTTT	3120
CCTTTTCTCT TTCTTAAAAA ATATGCTATA ATAGAGAGTA AAAAAGTTTG AAAGAAAGAA	3180
AAAGATGAAT TTAAGAGATT ACATTGCAAC AATTGAAAAT TATCCAAAGG GTACCG	3236

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2885 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

CCTGACTTTT CAAATTGGTT AGTTTGCCAC ACTTGGTTTA TATGCTCGTG GAAAGCATGG	60
CTATTACTTC TCAAAGGGCG ATTTCTCACC CCATGAAAAG TGTCTATTTT TGTTTAGGTT	120
TGTAAGTTAA TTCATTGTCA CATATTACTC TTAACTGAT TGAGTGAGTA CCGCTTATAT	180
TTGATGCCAA ACGCCTTAAA AGTGTACCC TCAAGTCCTT TTAGAATACG GCTATAATTC	240
CGCTCATTTT AAACATCTT AAGCTCATCA CTATCTAGGT TGGTATTAAA AATGGTATTT	300
TCACGATTGT TTAGCACGTC AAAGAGTAAA TCCTGCTCCC AGTCACTCTT AGGCTTAATA	360
ACAGCATTTT TTGCTCCTAA ATCATCAATA ATTAAGTAAT CAACAGACTT CATGAGTTCA	420
GTAGCTTCAA ACTCTGTAAG TGTTGCACCT TTACCATAAT TCCACCCCTC TTAAATTGT	480
TTGATCATTT CCGTTAGGCT TACAAAAAGC AACTCTTAG GTTCTCCTTT TGTCTTATAC	540
CCCTCATTTA TACCTTTGGC AATAGCAACT GATAAAAGTG TTTTTCCTT CCCTGTACCT	600
CCTGTGATAA GCGTATTTCC CCTCATGCCA TCAAGATATT TTTGTACCTG ACCTTTTGCA	660
AATCTAAAA ATCGCTTTTC TTCTGATGTT ACAGCATTAA AATCATCAA AGTTTTAGTT	720
TTAAACTCAT CTGCTACATA GCTCTTATTG CTCATCAACA CATTATAAGT TTGCATATAT	780

1236

AGTTTAGCAT TCAAATTATC AGCAATCGCA TCTTCTTCAT CTTGCTTTT CTGTTCTTCT	840
TGGCATTGTT CACAATAGGG TGGGATACAG CGAACTTCTT TTATTGCCTC TCCGTTCTCA	900
TTCCACCCCA CTACTACATG TCTTCTCCTT TTGATTGTG TTAGCTGTAT TTCATGCTTA	960
GGACACAATT CGTCTAGTTT AAATGTCTCA ATATTTCCCTA AACTAGATTG TAATGATTTT	1020
ATTTTCTGAC CTCCTAAAAT GGTTTTCTT GTGTTGGTAT CCAATCTTCA TAGCTGGTAG	1080
GCTCTAGTTG ATTGGTTTGC TGTTTTTTAG CCTCACGCGC TGCCCTGCTA TTTCTAACAA	1140
GTTCCACCGT CAATAAATTG TCCTGTTTCC AACGGTTAAG GATTACCTTG ATGTATGCAA	1200
AGTTTGCTTT ACCCTGACTG ACAGCCTCTT TTAACGCCTC ATGGATAAGC TCTGGGCTAA	1260
AATCTTCTAG CATATACTGC AATCTTGAA TCTGTAACGG TGACAAATGCT TTACCTGTCT	1320
CAGCTCGCTT CATATTCAAC AAGTCGTCTA TTTCCACACT GGTTACTTTT TTATTTACAA	1380
AATCAGAAAT CAGTTGAAAA ATGTTTGGAC TTTGTAGCTG GATTTTCAGCC ATTACCTCAT	1440
CAAATCTGTC TTGTGTCATG TTGTCTAAAT CTAGTGTCTG TGCATTGCCT CCTCAAACCT	1500
CTCTATAAGA CAACTTTTAT TTGCTTTCTG AGTTCATTT TTAGAGTTAA AAAGAATATC	1560
TTTTAAGGTT ACAGTAGCCT CTAAATACTC CTTTTAGCA TGCTCTATAT ACGCCTGTTG	1620
CTCTGCTTCG TTCTCAAAAA AGTGCTTAGC TTGGCGTTTA AAGAATGCTT TTCGCATAGC	1680
GTCCATTTCA AAAATACCAG GGGCGAAAAA CATTCCCGTA GTGCTTTTAG AGACCGCTTC	1740
GATTTTATGG CTTTCATTCA ATTCAGGAAG TTCAATCCAA AGTAAACGGG ACAACTCATC	1800
TTTGATGGAT TTTGTCTGAC TTTCCAATAA AGAAAGGATT CTTAGGCCAT TTTCTTCGCT	1860
AATTTCTCGC ATTTCTGCGC TAATCTGTC TATACGTCTA GTTAAATTCT CATATGTTGT	1920
TTCTGTCATG TTTTACCTC TGTTCCTTTG TTGGTGTGAT TTTTLAGCTT ATTTTTTTAC	1980
TTCTAAACAT CATGTCTTA ATTCCTGAT AACTCATTTT CAATTCAATC ATAGCTATTG	2040
CCATATCCTC AAATGCCTGG TACTGCTCCA ACTCCTCACT AGTCAAGCTA TCGATACCGT	2100
TATAGCCCCC ACGCTCTTCT CTTAACTGCT TAGCGTTCAT GTCTGTTACT GCCTTTAGTA	2160
GCAAGTTGTT CATGGTGCTA TGC GCGTGCT TTGGTGCAAT AGGCCATGTT TCTATACTGT	2220
CATGCAAGGT TTTTCTTTT CTTTCTTCTA GCGCCCTCTG CAGACGAATT TCAGAAAGTT	2280
CCTCACGCAT TTCAAAGAAT GCTTTGACTA GGTTTAGTTT GAATTGCCGT ACTGTTTCGG	2340
TATTCTTTAA ATAAGTGATC AGAAAAGTAG CCTGTTGCTC GTTCAGAATA TAGGATTTTT	2400
TAGGTTGTCC TCTAGTATCT AATTTATGGA TTTTAAATCC AAGTATTCCT AACTCTTCAA	2460
AGTCAGCCTT ATTTCTCTT ATTAAGCGCG TGATAGTGTG GTGTTGTACT TCAGCACATT	2520
CAGCGATGAT CTCGCTTGTG GTGTACGGCT CTTTCTTACC GTCCATGTAA ACTAGTTCCA	2580

1237

TTACGGTTCT ACCTCCTGTA TAAATCTGGT TAGCTTACTT TTTAATTGCC TCCTCTAGCC	2640
TCTTTTTTAG CCTCTAAAAC GGCTTTGGCT AGTGGTTAAT ATTATTTACC ACTTGTCTCT	2700
ATAAACGTGT TAGAGGCCTT TATAACGACT TGTATCGCTG TATCGATATC CTCCGTGGAA	2760
TAGTAGATTT ATTTTCTAAT ATCATTCAG ACTTGTTTAA CCCATTTCTT GAAAGAAATA	2820
AAATTACATC TTCTTTATCC TTGGCATCTG CTTTGTCTGA GACAAATTAG AATGTCAATA	2880
CTTGG	2885

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3144 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

TATCAATCCT TTCCCATAT AGGAGCAACA GAGTGGGAGT AGTCATCTAA GGAATAATTT	60
ATGTATTTTT ACGAGTCAGT ATCTTGGGAT ACTGGTTTTT ACTTTTCTAG ACTTTTGTAC	120
TACTTGTTAA AACTGGGATA ATTTTCGACT GTTTAACAGT TATTATGCAA AGTCTAAAAG	180
ATTAGAATTG TCAAAACAAT CCGTCTAGGC TTGATTTTAT CCTTTATTTA CTATAAAATG	240
AGAAGGAAAA ATGTCAAACT TTTATATTGC AAATAGGAGA AATCATGACA AAAACATTAA	300
AACGTCCTGA GGTTTTATCA CCTGCAGGCA CTTTAGAGAA GCTAAAGGTA GCTGTTCAGT	360
ATGGAGCAGA TGCTGTCTTT ATCGGTGGTC AGGCCTATGG TCTTCGTAGC CGTGCGGGAA	420
ACTTTACTTT CGAACAGATG GAAGAAGGCG TGCAGTTTGC GGCCAAGTAT GGTGCCAAGG	480
TCTATGTAGC GGCTAATATG GTTATGCACG AAGGAAATGA AGCTGGTGCT GGTGAGTGGT	540
TCCGTAAACT GCGTGATATC GGGATTGCAG CAGTTATCGT ATCTGACCCA GCCTTGATTA	600
TGATTGCAGT GACTGAAGCA CCAGGCCTTG AAATCCACCT TTCTACCCAA GCCAGTGCCA	660
CTAACTATGA AACCCTTGAG TTCTGGAAAG AGCTAGGCTT GACTCGTGTC GTTTTAGCGC	720
GTGAGGTTC AATGGAAGAA TTAGCTGAGA TCCGCAAACG TACAGATGTT GAAATTGAAG	780
CCTTTGTCCA TGGAGCTATG TGTATTTTAT ACTCTGGACG TTGTACTCTT TCAAACCACA	840
TGAGTATGCG TGATGCCAAC CGTGGTGGAT GTTCTCAGTC ATGCCGTTGG AAATACGACC	900
TTTACGATAT GCCATTTGGG AAAGAACCTA AGAGTTTGCA GGGTGAGATT CCAGAAGAAT	960
TTTCAATGTC AGCCGTTGAY ATGTCTATGA TTGACCACAT TCAGATATG ATTGAAAATG	1020



1238

GTGTGGACAG TCTAAAAATC GAAGGACGTA TGrAGTCTAT TCACTAyGTA TCAACAGTAA	1080
CCAACTGCTA CAAGGCGGCT GTGGATGCCT ATCTTGAAAG TCCTGAAAAG TTTGAAGCTA	1140
TCAAACAAGA CTTGGTGGAC GAGATGTGGA AGGTTGCCCA ACGTGAAGTG GCTACAGGAT	1200
TTTACTATGG TACACCATCT GAAAATGAGC AGTTGTTTGG TGCTCGTCGT AAAATCCCTG	1260
AGTACAAGTT TGTCGCTGAA GTGGTTTCTT ATGATGATGC GGCACAAACA GCAACTATTC	1320
GTCAACGAAA CGTCATTAAC GAAGGGGACC AAGTTGAGTT TTATGGTCCA GGTTCCTGTC	1380
ATTTTGAAAC CTATATTGAA GATTTGCATG ATGCTAAAGG CAATAAAATC GACCGCGCTC	1440
CAAATCCAAT GGAAGTATTC ACTATTAAAG TCCCACAACC TGTTCATCA GGAGACATGG	1500
TTTCGAGCTCT TAAAGAGGGG CTTATCAATC TTTATAAGGA AGATGGAACC AGCGTCACAG	1560
TTCTGTGCTA ATGTAGTTGT TTAGTTTAA AAAACTATGC AAAGCTCCAT ATACAACACT	1620
TAAACGAGAT TAAAGAATGG CGAAATCCCT TGATGCGCAA GAGATTAGCT GTCTTTTTTA	1680
TTTTTTAAGT GATAAAGTCG GAGTTTAGGC ATCAAAGCCT ATCAAATTAA ACAAAGAAGC	1740
GATGTCTTAG ATATTTTGAA AAAAATTAAT AAGCAGAAAA CTCTCTATTA TTTTGTGTGA	1800
GAGAGTTTTT TGTTAATAAA ATTTACAAA ATGACATTA TATATTGCAT TAAGTTAGAT	1860
ATATGATATA ATATTGTAA AAAGAGGCGC AACTTTTAA AATTAATGAG AATCAAAGAG	1920
AAAACCAATA ATATTAATGG AGGAATAAAA AATGTAAGTA AGCATTATGG TCATTCAATC	1980
ATTCTCAAAG ATATAAATTT TGCACCTAAC AAGGGTGAAG TTGT'TGGTCT AGCAGGGAGA	2040
AATGGAGTTG GTAAGAGTAC GTTGATGAAA ATTCTTGTTT AGAATAATCA ACCGACTTCA	2100
GGTAATATTA TAAGCAGTGA TAATGTTGGG TATTTAATCG AAGAACCAAA ATTATTTTTA	2160
TCATAAACAG GTTTAGAGAA TTTAAATAT TTGTCAAAT TATATGGTGT TGAATACAAT	2220
CAAGAAAGAT TTAGATGTTT GATCCAAGAG TTAGATTGA CTCAGTCTAT TAATAAAAAA	2280
GTAAAGACCT ATTCITTTGGG TACAAAACAA AAATTAGCTT TGC'TTCTAAC TCTCGTTACG	2340
GAACCTGATA TATTGATTTT AGATGAACCG ACTAATGGTT TAGATATTGA ATCATCACAA	2400
ATAGTTTTAG CGGTTCTAAA AAAATTAGCT TTACATGAAA ATGTGGGAAT TTTAATATCG	2460
AGTCATAAAT TAGAAGACAT TGAAGAAATT TGTGAGAGAG TTCTTTTCTT GGAGAACGGG	2520
CTTTTGACAT TTCAAAAAGT AGGAAAAGAT AGTCATAATT TCTTGTTTGA GATAGCTTTT	2580
TCATCAGCTA CAGATAGAGA CATTTTCATT ACCAAACAAG AATTTTGGA TATTGTTTAG	2640
GAAGAGGGAT TGAGAATTAC TATGTCTGGG AATATTCAAA ATAGTGAGCT TTTTAAATTT	2700
TTTAACGAAA ACTCTATTAA AGTAGTTGAT TTTGAAACTA AAAAAGAGAC GCTTAAAGAT	2760
ATTTACCTAA ATCGTTCAAA ATAAAGGAAG GTTATAATCA TGAAATTAAA TAAACAGAAG	2820

1239

AATCGGATGA TTTACGTCTT GTCTAATTTT CTATATGCTA TCTCAGTTTC CATTATTTAT	2880
GCTTTGAATG GCATTGTGTT ACTAGTCATA GTAAGTAAAT TGGGTATTCC AGGTGATTTA	2940
GGATTAAATT TTATAGTAGC TATTGTAGTC AATACAATTT TGTTAGTCCT GTTTTATTTT	3000
CTATTATCTT ACATTTTCTA TTTATACAAA TTGAAAAGTG GCTTGGTATw TGGTATTTTA	3060
GTAGCTTTAC TACTCTTTAT CTCTAATATA TTAAATACGA TGATGATGAA TACTAGTAAT	3120
GATTTGTTTA TCAAAGCAAT TGAA	3144

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3766 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TACGGTATTA TTTTAAAGGA GAAAGAATCA TGAAAATCAA AAAATGGCTT GGTCTAGCAG	60
CCCTTGCTAC AGTCGCAGGT TTGGCTCTTG CAGCTTGCGG AAATCAGAA AAGAAAGCAG	120
ACAAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG CGGTTCTGAA GAAAAACGTT	180
GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC CTTGGAA'TTT' ACAGAGTTCA	240
CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA AGTAGATTG AACGCTTTCC	300
AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG AAAAGACCTT GTAGCGATTG	360
CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT GAATGGAAGT GCCAACAAGT	420
ACACTAAAGT AGAAGACATC CCAGCAAACG GAGAAAATCGC TGTACCGAAT GACGCTACAA	480
ACGAAAGCCG TGCCTTTTAT TTGCTTCAAT CAGCTGGCTT GATTAAATTG GATGTTTCTG	540
GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC AAAGAACTTG AAAATCACTG	600
AATTGGACGC TAGCCAAACA GTCGTTTCAT TGTCATCAGT TGACGCTGCC GTTGTAACA	660
ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC ACTTTTCAAA GAACAAGCTG	720
ATGAAAACCTC AAAACAATGG TACAACATCA TTGTTGCAAA AAAAGATTGG GAAACATCAC	780
CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA CACAGATGAC GTGAAAAAAG	840
TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG GTAATAAGAA ACAGGGAGGT	900
GGGAGAGAAA ATTCCACCTC TTGCTTTTGT ATAGAGTATA GATTGTAAAG AAGACTATTC	960
GTTCATAGAA AGGTAGAGAG AATATGGTTT TTCCTAGCGA ACAAGAACAG ATTGAAAAAT	1020

1240

TTGAAAAGGA TCATGTAGCC CAGCATTATT TTGAGGTTTT GCGTACCTTG ATTTCTAAGA	1080
AATCAGTCTT TGCCCAGCAG GTTGGACTCA AGGAAGTCGC AAATTATCTG GGTGAGATTT	1140
TCAAGCGTGT TGGAGCTGAA GTGGAGATTG ATGAGAGCTA TACAGCGCCC TTTGTCATGG	1200
CACATTTCAA GAGTTCGCGT CCAGATGCCA AGACCTTGAT TTTCTATAAC CACTATGACA	1260
CTGTGCCAGC GGATGGGGAT CAGGTCTGGA CAGAGGATCC kTTTACGCTT TCGGTCCGCA	1320
ATGGCTTCAT GTATGGGCGT GGGGTGTGATG ACGACAAGGG TCATATCACA GCTCGCTTGA	1380
GTGCTTTGAG AAAATATATG CAGCACCATG ATGATTTACC TGTCAATATC AGCTTTATCA	1440
TGGAGGGAGC GGAGGAATCG GCTTCAACAG ACCTAGATAA GTATTTGGAA AAGCATGCAG	1500
ACAAACTCCG TGGGGCGGAT TTGTTGCTCT GGGAAACAAG GACCAAAAAT GCCTTGAAC	1560
AGCTGGAAAT TTCTGGTGGC AATAAGGGGA TTGTGACCTT TGATGCCAAG GTAAAAAGCG	1620
CTGATGTGGA TATCCACTCG AGTTATGGTG GTGTGTGGA ATCAGCTCCT TGGTATCTCC	1680
TCCAAGCCTT ACAGTCTCTT CGTGCTGCGG ATGGCCGTAT CTGCTTGAA GGCTTGACG	1740
AAGAAGTACA AGAGCCCAAT GAACGAGAAA TGGCCTTGCT AGAAACTTAT GGTCAACGAA	1800
ACCCAGAGGA AGTTAGTCGG ATTTATGGAT TGGAGTTGCC TCTCTTACAG GAGGAGCGGA	1860
TGGCCTTTCT AAAACGTTTC TTTTTCGATC CAGCGCTTAA TATCGAAGGA ATCCAGTCTG	1920
GTTATCAAGG TCAGGGTGT TAAAGACTATTT TACCTGCAGA AGCCAGTGCC AAGCTAGAGG	1980
TTCTGCTGGT TCCGGGCCTA GAACCGCATG ATGTTCTGGA AAAAATTCGG AAACAGCTAG	2040
ACAAAAATGG CTTTGATAAG GTAGAATTAT ACTATACCTT GGGAGAGATG AGCTATCGAA	2100
GCGATATGAG CGCACCAGCC ATTCTCAATG TGATCGAGTT GGCCAAGAAA TTCTATCCAC	2160
AGGGCGTTTC AGTCTTGCCG ACGACAGCGG GGACAGGACC TATGCATACG GTCTTTGATG	2220
CCCTAGAGGT ACCAATGGTT GCATTTCGGTC TAGGAAATGC CAATAGCCGA GACCACGGTG	2280
GAGATGAAAA TGTCCGAATC GCTGATTATT ACACCCATAT CGAATTAGTA GAGGAGCTGA	2340
TTAGAAGCTA TGAGTAGAGA TATTATCAAG TTAGATCAGA TCGATGTGAC TTTTCACCAA	2400
AAGAAGAGAA CCATCACAGC GGTTAAGGAT GTGACCATTC ACATCCAAGA AGGGGATATC	2460
TACGGAATCG TTGGATATTC TGGAGCAGGA AAATCAACCC TTGTACGGGT GATTAATCTC	2520
TTGCAAAAAC CATCTGCAGG GAAAATTACC ATTGACGACG ATGTGATTTT TGACGGCAAG	2580
GTGACCTTGA CGGCAGAGCA GTTGCGTCGT AAACGTCAAG ATATCGGAAT GATTTTCCAG	2640
CATTTTAACC TGATGAGCCA AAAGACAGCA GAGGAGAATG TAGCCTTTGC CCTTAAACAC	2700
TCTGAACTCA GCAAGGAAGA AAAGAAGGCT AAAGTAGCTA AGTTGTTGGA CTTGGTTGGT	2760
TTGGCAGATC GTGCTGAAAA CTACCCTTCA CAACTATCTG GAGGGCAAAA ACAGCGTGTG	2820

1241

GCAATTGCGC GTGCCTTGGC CAATGATCCA AAAATCTTGA TTTCAGACGA GTCAACTTCT	2880
CCCCTTGATC CGAAGACAAC CAAGCAGATT TTGGCCTTGT TGCAAGATTT GAACCAAAAA	2940
TTAGGCTTGA CTGTTGTCTT GATTACGCAT GAAATGCAGA TTGTCAAAGA CATTGCCAAC	3000
CGTGTTCAG TTATGCAGGA TGGGCATTG ATTGAAGAGG GTAGTGTGCT TGAAATCTTC	3060
TCAAACCTTA AACAACTTT GACTCAAGAC TTTATCTCAA CAGCTACAGG TATTGACGAA	3120
GCCATGGTCA AAATCGAGAA GCAAGAAATC GTGGAACACT TGTCTGAAAA CAGTCTCTTG	3180
GTGCAACTCA AGTACGCTGG AGCTTCAACA GACGAGCCAC TTTTGAATGA ATTGTACAAG	3240
CATTACCAAG TAATGGCTAA TATTCTCTAT GGGAATATCG AAATTCTCGA TGGTACTCCT	3300
GTTGAGAAT TGGTGGTGGT TTTGTCAGGT GAAAAAGCAG CGTTGGCAGG TGCCCAAGAA	3360
GCCATTCGTC AAGCAGGTGT ACAACTAAAA GTATTGAAGG GAGTACAGTA AGATGGAATC	3420
ATTGATTCAA ACCTATTTAC CAAATGTCTA TAAGATGGGT TGGGCTGGTC AGGCAGGCTG	3480
GGGAACGGCT ATCTACTTAA CTCCTTATAT GACAGTTCTT TCCTTCATTA TCGGAGGCTT	3540
CTTGGGGCTA GTGGCAGGTC TCTTCTCGT CTTGACAGCG CCAGGTGGTG TCTTGGAGAA	3600
TAAAGTCGTA TTCTGGATTT TAGACAAAAT TACCTCAATT TTTCGTGCGG TTCCCTTTAT	3660
CATCCTCTTG GCAATCTTGT CACCACTTTC TCACTTGATT GTTAAACAA GTATCGGGCC	3720
AAATGCAGCC CTGTCCAC TTTCTTTTGC AGTCTTTGCC TTCTGG	3766

(2) INFORMATION FOR SEQ ID NO: 226:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2520 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

TGTTGCTGAG TTAATCGGTA CGTTCATGTT TGTATTCGTC GGGACAGGAG CTGTTGTTTT	60
TGGAAATGGT CTTGATGGCC TTGGTCACCT TGGAATCGCC TTGCTTTG GTTTGGCAAT	120
CGTGGTGGCA GCCTACTCAA TCGGAAGTGT TTCAGGTGCT CACTTGAACC CGGCTGTTTC	180
GATTGCTATG TTTGTAAACA AACGTTTGTG ATCTTCAGAA CTTGTAAACT ACATCCTTGG	240
TCAGTTGTT GGAGCTTCA TCGCTTCTGG CGCTGTCTTC TTCCTCTTGG CTAATCAGG	300
TATGTCAACT GCTAGTCTTG GTGAAATGC CTTGGCAAAC GGTGTCAC TGCTTTGGTG	360
TTTCTTGTG GAAGTCATCG CAACTTCTT GTTGTATTG GTTATCATGA CTGTGACTTC	420

1242

AGAAAGCAAG GGCAATGGCG CGATTGCTGG TTTGGTAATC GGTTCGTCAT TGATGGCGAT	480
GATTCCTGTC GGATTGAAGA TTAGTGACT TTCAGTAAAC CCAGCTCGTA GCTTGGCACC	540
AGCTGTCTTG GTAGGCGGCG CACCTTCAA CAAGTTTGGA TTTTCATCCT TGCACCAATC	600
GCTGGTGGAG TTCTTGCAGC CCTTGTGCA AAAAATTCC TTGGAACAGA AGAATAATTG	660
AAACTCAAAA AGCCTTGCTC CTCATCTTGA GGAACAGGGC TTTTTCGTAT GATACTCTTC	720
GAAAATCTCT TCAAACCACG TCAGCTTCAT CTTGCCGTAG TATGGTTACT GACTTCGTCA	780
GTTCTATCCA CAACCTCAAA ACAGTGTTTT GATCTGACTT CGTCAGTTCT ATCTGCAACC	840
TCAAAACAGT GTTTTAAGCT GACTTCGTCA GTTCTATCTG CAACCTCAAA ACAGTGTTTT	900
AAGCTGACTT CGTCAGTTCT ATCTGCAACC TCAAAACAGT GTTTTAAGCT GACTTCGTCA	960
GTTCTATCTG CAACCTCAAA ACAGTGTTTT AAGCTGACTT CGTCAGTTCT ATCCACAACC	1020
TCAAAACAGT GTTTTGATCT GACTTCGTCA GTTCTATCCA CAACCTCAAA ACAGTGTTTT	1080
GATCTGACTT CGTCAGTTCT ATCCACAACC TCAAAACAGT GCTTTGAGCA ACCTGCGGCT	1140
AACTTCCTAG TTGCTCTTT GATTTTCATT GAGTATGACT TTAGCGGTG TCAATTTTCT	1200
CTGGATAAAG GTCGTGTTGG AAGAGCGGTT GTTCGCCAA GCCCTCATAC TTAGTTCCTT	1260
GCTTACCGTA GTTGTAGTAG GGGTCGATTG AAATGCCACC GCGCGGAGTG AATTTTCCCC	1320
AGACTTCTAA ATAGCGAGGG TCTAGCAAGT TGACCAAGTC TTTCCCGATG GTGTTGATAC	1380
AGTTTTCTG GAAATCTCCG TGGTTTCGGT AGCTAAATAG ATATAGTTTG AGGGATTTTG	1440
ACTCGACACA GAGCTTGTCA GGAATGTAGG AAATATGAAT CGTCGCAAAG TCTGGCTGAG	1500
CAGTGATTG TCCCAGCAGA GACATATCGA GGATATGGTG ACGAATGCCC TGTTCTTAG	1560
CGATTTCTCT AGTAATTTGA ATTTGAGGT GATGACGTTG GCCGTAGGCA AAGGTGACAG	1620
CTTCGACTGT TTCATAGTGT TGCATGACCC AGAAAAGGCA GGTTGTTGAA TCTTGACCAC	1680
CACATAAGAC GACCAAGGCT AATTGACGTT TCATAGTACT CCTTCCAAA TGGGAAATGT	1740
TCAGAGCAG CAAAAAGCTC CCATTAGGGA GCTAAAAAAT ACCAAATCGA GGTTTTTTTA	1800
GCGATGGCAT ATCCCAAACA TCGTAATATT CTACTTATAT AGTAAATGA AATAAGAACA	1860
GGACAAATCG ATCAGGACAG TCAAATCGAT TTCTAACAAT GTTTTAGAAG TAGAGGTGTA	1920
CTATTCTAGT TTCAATCTAC TATAGTCTAG CATATTTTTT GAAAAATGGC AAAGGGCAAG	1980
AAAAAGAGA CCAAAGAAAG TACTTGGTCT CTCGTTTGAT TAGCTCAATT CAGCAATGAT	2040
GGCCTTGATT TGTTCGTG TGTGAACACC TGCAACTTGT TTGACAACTT GGCCGCTTTT	2100
TTTGAAGAGA AGAGTTGGAA TAGACATGAT TCCAAAAGCA CGAGCTGTGT TTGGATTTTC	2160
ATCAACGTCC ATTTTAACGA TTTTCAAGAC ATCTTCTGAA AGTTCCTCAG ACAATTTGTC	2220

1243

CAAGATTGGA CCTTGCATAC GACATGGACC ACACCAAGTT GCCCAGAAGT CTACTAAGAC	2280
CAAACCGTCT TTTGTTTCTT GTTCGAATGT TGCATCTGTA ATTGCTTTTG CCATTGTATT	2340
TCTCCTTTT TTAGTTATAT TGGCTTAAAT CTTGTTTCAT GAGATAGAAG AAGATATCTC	2400
CATAAGTCCC ATGGTAGTCC AAATTATGAC CTTGTAAGT TAATTTTGG ACAGGGTAGT	2460
AkkCTGCGAC GCCGATAAGG CAAGCTTGTT GCGAACGTTT AAAGTCTTCA TAAGACTCGG	2520

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5278 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

ACTCAGTTAG ATTTTGT TTTT CAAAAACAAC GAAGAAAAAG ACCATGTTGC TCTACTTGGA	60
AGAATTGGCT CCGAACGTGT TTATCGATAT ATTAATAAAA AATATTTAGA TTTACCGGAA	120
ACATTCGAAA ATTATAATGT TTTGTACCA GAAGCTAATG GAAGTGGTGC CTTAGGTGAA	180
GTCTTATCAA CACCCTAAT CGGGGAACCC CTAATCGGGC ATACAGATAC TTTTATCT	240
ATTGGTAATT TTAACAACA ATTTGAAGCC GATGCTTGTA TTAAATTTAT TAAACTAAA	300
TTGCTAGAG TATTATTAGG TGTTTGAAG GTTACTCAGC ATAATTCACG CAAACTTGG	360
TATTACGTCC CCCICCAAGA CTTTACGGTC AATTCGGACA TTGATTGGAC ACAATCACTG	420
ACTGATATTG ACCGCCAGCT TGATCAAAAA TATGACTTTT CCCCTGAAGA AATTGCCTTT	480
ATTGAGAATC ATGTAAGGGA GATGGATTAG AAAAGTATTT TTATTTGACA AATAGTGCTC	540
AATGATCTAA AATGACTATA TAGGATTAGC TCAGGAAGCA TACGATGCCC TGACCCTTTT	600
TGTAATTATG AGATGAGAAA GTCATTTGTT AGATAAATTG ACTCGTTAGC AAACGTTCAA	660
AAAAGGAAAA CTTATGCCAG TAGAAATTAA AACCCTAAA GAAATTCATC CTAAATCTA	720
TGCTACACC ACACCGACAG TAACCAAGTA TGAAGGCTGG ATTAAGATTG GGTATACAGA	780
ACGTGATGTC ACACAACGTA TCAAGGAGCA AACGCATACA GCTCATATAG CTACAGATGT	840
CTTATGGACT GGTGATGCAG CTTATACAGA AGACCTGAT AAGGGGAAAA CTTTCAAGGA	900
CCATGATTTC CACCATTTC TTTCTTTCCA TGATGTAGAA CGTCGTCCCA AGACGGAATG	960
GTTCTATTTT AATGGAATC CTGAAAAATC AAAAAATCTT TTTGATAAGT TTGTTTCAAGCA	1020
TGATTTGTCT GGTATACAGC CTGAAAAAGG ACAGGACTAT ACTCTGCGAC AAGAGCAAGA	1080

1244

AGAAGCAGTT GCTAAGACAT TAGCTTATTT CCAAGAACAT GCTGGAGGCA AGTTTCTCTG	1140
GAATGCCAAG CCACGCTTTG GTAAAACCTT GTCTACCTAT GACCTAGCTC GACGGATGGA	1200
AGCTGTCAAT GTCCTAATTG TAACAAACCG CCCTGCCATT GCTAACTCAT GGTATGATGA	1260
TTTTGAAACA TTCATAGCAG GTCAAACGAC TTACAAGTTT GTTCTGGAAT CAGATAGCCT	1320
TAAGAGTCGT CCAATCTTGT CACGACAAGA ATTTCTTGGT ATTTTAGCTG ACGATGTAAG	1380
ACAACTTGCT TTTATCAGTC TCCAAGACTT GAAAGGATCT GTTTATTTAG GTGGAGAGCA	1440
CGATAAACTC AAATGGGTAA CTGATCTGCA TTGGGACTTG TTGGTTATTG ACGAGGCTCA	1500
TGAAGGAGTT GATACCTTCA AGACTGACCA AGCCTTTAAT AAGATTCGAC GAAATTTTAC	1560
TCTGCATTTG TCAGGTACAT CATTTAAAGC ATTGCGCTAA GGAGATTTTA CAGAGGAACA	1620
AATCTACAAC TGGTCTTATG CTGATGAGCA GGCTGCTAAG TATTCGTGGT CTCTTGAGCA	1680
AGAAGAGGAA AATCCTTATG AAAGCTTGCC TCAGTTGAAT CTCTTACCT ATCAAATGTC	1740
TCAGATGATT GCGGAAAAGT TAGAAAAAGG CGCTCAGATC GATGGTGAAA ATATTGACTA	1800
TGTTTTTGAC TTAAGTGAAT TTTTCGCTAC AGATGATAAA GGGAAATTTA TTCATGAGCA	1860
TGATGTCAGA AATTGGTTAG ATACTCTATC AAGCAATGAA AAATATCCAT TTCAACCAA	1920
AGAAGTCCGT AATGAAGTCA AGCATACTTT TTGGCTTTTA GAACGTGTCG CTTCGGCCAA	1980
AGCATTAATA GCCCTACTAG AAGAACACCC AATCTATGAA AACTATGAGA TCGTTCTAGC	2040
TGCTGGTGAC GGACGTATGT CCGAAGAAGA CGATAAAGTC AAACCAAAT CCTTGACTT	2100
GGTTAGAAAA GCGATAGCAG AGAATGACAA AACCATTACC CTATCCGTTG GTCAGCTGAC	2160
GACAGGTGTC ACTATCCCTG AATGGACAGG TGTATTGATG TTATCAAATT TGAAATCACC	2220
AGCTCTTTAT ATGCAGGCCG CCTTCCGTGC TCAAAATCCT TACTCATGGA GCGATAACAA	2280
AGGAAATCAC TTTCGCAAAG AAAGAGCCTA TGTATTTGAC TTTGCGCCG AAAGAACCTT	2340
GATTCTCTTT GATGAGTTG CCAACAACCTT ATTGCTTGTA ACTGCAGCTG GTAGAGGAAC	2400
TTCAGCTACA CGCGAAGAAA ATATTAGAGA ATTATTAAC TTCTTTCCAA TTATTGCCGA	2460
AGACCGTGCT GGTAAAGATG TTGAAATTGA TGCAAAGGCA GTTCTAACCA CTCCTCGCCA	2520
GATAAAAGCT AGAGAAGTTC TTAAACGAGG TTTTATGTCC AATCTCTTAT TTGATAATAT	2580
TAGTGGTATT TTCCAAGCAA GTCAAACAGT TTTAGATATT TTAAATGAGC TGCCAGTTGA	2640
AAAGGAAGGG AAGGTACAAG ATAGTTCTGA TTTATTAGAT TTTTCAGATG TTACAGTCGA	2700
TGATGAGGGA AATGCAGTAG TAGACCATGA AATTGTAGTT AATCAGCAA TGCGACTTTT	2760
TGGTGAAAAA GTTTATGGAC TTGGTGAATC TGTGCTGAG TTAGTCACAA AAGATGAGGA	2820
ACGAAGTCAA AAACAGCTGG TCAATGACTT GAGTAAGACC GTTCTTTCAG TGATTGTAGA	2880

1245

GGAATTGAAA GCAGATTATT CTCTAAAAAC AAGGGAAACT GAGCAAATTA AGAAACAAAT	2940
TACAGCAACA CTTGAGAATG AAATTCGAAA AAATGATATC GAAAGAAAAA TTTCTGAAGC	3000
TCATATCAAG CAAGAGTTGC AACAGCAGCT CAAAGAAGCA AATGATAAAG CGCAAAAAGA	3060
TAAGATTCAA GAAGATTGCG AAAAACGTTT AGAAGAAAAA AAACTCATTC ATAAAGAAAA	3120
ACTAGAACAA AACTCAAAA AAGAAGTGGA AAAAATGCCT GAGAAATTTA TCGAACAGGT	3180
TGAGATAAAA CGTGTGGAAC AGTTGAAACA ATCAGCTCAA GATGAAATTC GTGACCATTT	3240
ACGAGGGTTT GCAAGAACAA TTCCAAGTTT TATTATGGCT TACGGTGATC AAACCTAAC	3300
ACTTGATAAT TTTGATGCCT TTGTTCTGTA ACATGTTTTT TATGAAGTAA CAGGGATTAC	3360
GATTGATCAG TTTAGATATT TGCGAGATGG TGGGCAGGAT TTTGCAGGGC ATCTCTTTGA	3420
TAAAGCAACA TTTGACGAAG CTATTCAAGA ATTTCTTCGC AAGAAAAAGG AGTTGGCGGA	3480
TTATTTTAAA GATCAAAAAG AAGACATTTT TGAATATATT CCACCGCAGA AGACCAACCA	3540
AATTTTCACT CCTAACGAG TGGTGAAAAG GATGGTAGAT GATTTGGAAG AGGAAAAATCC	3600
AGGGATTTT GATGATCCAT CTAAGACTTT TATTGATTTA TATATGAAGT CAGGCCTCTA	3660
TATTGCAGAA CTTGTGAAGC GGTTATATAA TAGCAATGGC TTGAAAGAGG CCTTTCCAAA	3720
TCCTGAAGAA CGCTTAAAC ATATTTTGGG AAAGCAAGTT TATGGATTTG CTCCGTCTGA	3780
GATTATCTAT AACATTTCCA CTAATTTTAT ATTTGGCAAT CTTTCTAAAG ATATCAGTAG	3840
GAAGAAATTT GTTTTAGCAG ATACCATTTCC AGCGGCTAAA GAAGGGAGCA TTCAAAAGTT	3900
GGTTGATTCC TATTTTGAAA ATAATTAATA AGAAGGCCGA GTCAAAATTC TTTGAAATCA	3960
GAAAAACGC ATAATATTGA GTGCTTTTGT ACTGCCCCC AAAAGTTAGA CAGAAAAAAT	4020
CTAACTTTTG GGGGCGAGT CAGACAATCC TTGGTATTAT GCGTTTATT GTGGGAAGAT	4080
GTATAATGGA TTGAAATAAG ATATGAACAA ATCAATTAGG AATTTAAAGC ATTTTATAAC	4140
AACGTTTGTAG AGTAATGGGG GGCTATTTCA ACTTCAACCT ACTATAATAC AGAAAAAAC	4200
AACTCCCTGA TAATTCAAGG AGTTGTCTAT AGTTAAATTA GTTTTGTAGG GCTTCTTGGA	4260
ATTCTGGGTT TTTCCATGCT TCGTCAATGA TAGCTTGTA TTTCTTAGCA GATGCTTGCA	4320
TTTTTTGAGT TTCTGCGTCG TTCAATGGGA TATTTACTGG ACGAACGATA CCATGTGCAC	4380
CAACAACAGC TGGTTGACCG ATAAAGACAT TCTCAACTCC GTATTGACCT TCTTGAATA	4440
CTGAAAGTGG AAGTACTGCG TTTTCATCGT CAAGGATTGC TTTAGTGATA CGAGCAAGGG	4500
CTACTGCGAT ACCGTAGTAT GTTGACCTT TTTTGTGAT GATTGTGTAG GCTGCATCAC	4560
GAACACCTTC GAACAATTCA ATCAATTCAG CTCTTGAAC ATTTTGAGTG TCTTTAAGGA	4620



1246

ATTCTTCAAG GTTTACACCA GCGATGTTAG CGTGTGACCA AACAGCGAAC TCAGAGTCAC	4680
CGTGTTCACC CATGATGTAG GCGTGCACGT AACGAGCATC CACATCCAAT TTTTCAGCAA	4740
GTGCTTGACG GAAACGAGCT GAGTCAAGTG AAGTACCTGA ACCGATAACG CGTTCCTTAG	4800
GGAAACCAGA GAATTTCCTAA GTTGAGTAAG TCAAAACGTC AACTGGGTGA GCAGCAACAA	4860
GGAAGATACC TTTGAAACCA GATTCAACAA CTTGAGTTAC GATTGATTTG TTGATAGCAA	4920
GGTTTTTACC TACAAGGTCA AGACGAGTTT CACCTGGTTT TTGAGGTGCA CCTGCAGTGA	4980
TCACAACAAG GTCAGCGTCT GCACAGTCAG AGTATTGAGC TGCATAGATT TTTTtagGTG	5040
AAGTGAAGGC AAGGGCGTGA CTAAGGTCAA GCGCATCACC AACAGCTTTT TCATGCAATT	5100
GTGGAATTC GATAATTCCA AGCTCTTGTG CAATTCCTTG GTTACAAGT GCAAAGCGT	5160
AAGATGAACC TACAGCACCA TCACCGACAA GGATAACTTT TTTGTGTCT TTAGTTGAAG	5220
TCATTGTTTT AAACATCTCC TTAATTTTAT TAGGGGATTT TCCCTAGACA ACTTCATT	5278

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1941 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

ATAAGGAATC TCTAAAAAAT TTTAAGGAGA ATCTAGCAAA TGGATTTCAC ATGGGCACTG	60
AAGTATGCCA CTGAATTTTT GGAAGCTGCC ATTTTGATCA TTCTTGGGAA TGGTGCAGTT	120
GCCAAACGTTG AACTTAAAGG TACGAAAGGT CACCAAAGTG GCTGGATCGT CATCGCTGTT	180
GTTTATGGTA TGGGGGTTAT GATCCCAGCC TTGATGTTTG GTAACGTATC TGGGAATCAC	240
ATCAACCCCTG CTTTCACTCT AGGGCTTGCA GTTAGCGGTC TTTTCCCTTG GGCACAAGTG	300
GTACCTTACA TTATCGCGCA AGTCTTGGG GCTATCTTTG GCCAAGCCTT AGTTGTGGCA	360
ACATACCGTC CATTCTACTT GAAAACTGAA AACCCAAATA ACATCTTGGG AACTTTCTCA	420
ACTATTTCAA GTATTGACCA TGGTACAAAA GAAAGTCGCT ATGCAGCAAC TGTCAATGCT	480
TTGATTAATG AGTTTGTGG TTCATTGTGTT TTGTTCTTTG CAGCTCTTG TTTGACTAAA	540
AACTTCTTTG GTGCTGAAGT GCTTCAATTC ATGAAACAAA AGGCAACAGA AGCAGGACAA	600
ACAGTTGATT TTTCTGACTT GGCTATTAAA GCACAGGTGG CTCCACACAC TGCTTCAGGA	660
CTTCTGTGG CTCACTTGGC ACTTGGATTC CTCGTTATGG CTTTGGTAAC ATCATTGGA	720
GGACCTACAG GACCTGCCTT GAACCCAGCC CGTGACTTGG GACCACGTCT CCTTCATGCT	780

1247

TTCCTTCCCA AATCAGTTCT TGGTGAGCAT AAAGGCGATT CAAAATGGTG GTATTCTTGG	840
GTACCAGTAG TAGCACCTAT CGCAGCAGCA ATTGCGGCAG TAGCTGTATT CAAATTCCTT	900
TATCTCTAAG AAATAGCTCC TTTAACATTT GAGTGAGCAC CATCTATAAG TAAGAGAGGA	960
TCAGACTGGK TCTCTCTTTT kGATTTTtAG GGAAATGAAA GAACtCTAAA CAAACTCCTC	1020
TCCAGCAGTG GTTTAGAAGT CTCAGTGGGC TATTCCAGCT TCAATGGACT ATAGTAGGTT	1080
GCAGTTGAAA TAATAGACCC TTGTTTCTAA AACATTGTGA GAAATTGGTT TGAATTCtCC	1140
AATCAAATG TGCAGTTTTC ATTCTACTAT ATATTATCGG AATATTATCG GAGATGGGTT	1200
CCCTATCTTG TAAGTCTGCT TTATAGTGGG TTGAAGTTGG AATAGTCCTC CCTTCTTTCT	1260
CAACATTGT GAGGAATTGA TTtACCTTCC TCAACAAAAT GTTCAGTTTC TATTTcATT	1320
TACTATAAAA TAAGCGATTA GGGGGGCTAT TCTTCGACCT ACATTGACTC TGCTGAGTCC	1380
TATGATTGTT ATCGTTTTAT CTGCAATTTT ATACTCAATG AAAATCAAAG GGCAAActAA	1440
GAAGCTAGCC GCAGGTGTT CAAAACACAG TTTTGAGGTT GTATAGTAGA TTGAAActAG	1500
AATAGTACAC ATCTACTTCT AAAACATTGT TAGAAATCGA TTTGACTGTC CTGAACGATT	1560
TGCCCTATTC TTGTTTCATT TTACTATATA AACCAGAGAC TGTTTACATT TTCAGCAAGT	1620
GAGTGGATGG ATAATGCTGA AACTCCTTG AAGGATAAGT CTATTTAGTA CTTTCTATTA	1680
ATTAGTTAAA TTTTtACCAA GAATAATICA CAAAAACGTT GTAAAACACT TGCAATTTAG	1740
CTGAAATTTG ATAAAAAGT AAGGAAAGTT AGACTGTATT GCCTACTGTC TATCTATAAA	1800
ATATATTTTA TTGGAGGCTT TTACTCAAAT GGCAAAAGAA AAATACGATC GTAGTAAACC	1860
ACACGTTAAC ATTGGTACTA TCGGACACGT TGACCACGGT AAAACTACCC TAACTGCAGC	1920
TATCACAACT GTTTTGGCAC G	1941

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 755 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATTtGAAGAA ATTGAAGAAA TCGTAGCCCC TACAGATGGT GAATTTTTGG GGGAACTTTT	50
ACTTGGAAct GGGGTAGTTC TCTTAATTGG AGTAGCCTGT TGTTAAAAAG ATAGGGAGTG	120
ATAATCATGC AAGATAACTT TTTATTtGAG GAAATTGAAG AAATTTCAGT ACCAGTTAAT	180

1248

GATTTTTCAG CTGGACTTGC AACAGGTATC GGATTGGTT TAGCAATCCT TGCTCTTGCT	240
GGTTGTTGAA GTTTGTTTCAT TTAATAACAT CAAGCTTTTT CAATTTTCATT TTAGACAGTC	300
ATTTAAATTT TCCGTATTAG TCTTGCAGCA AGAGATTAAT AGAATTAGTC ATTATTTTAT	360
TGATTGCGGA CTGAGGGACT AGAGTATGTT TTAATAACC CCTCTTTTAT TTATTAAAGG	420
TTAGGTTTGT TATGAGAATT GTTGATAAGA TTAAGATATT ACCTACTCCT TATGAGGGAC	480
ACTATCATT ATATATACCA TCCAGTAAGA AACATGTATT AGTTGGGAAA CAGGAAAAAA	540
ATGGTTAGAG CAACTAATAG GTCAAGAATT TACCATATCG GACTTATTAG TGTAGTAGG	600
GAAGAAATAT TTTTAAATA TCTTGGGACT TTAATATAAC ATTATCTGAA AAATTAAACT	660
ATAAAGATT TAATAAGAAT TTTGAAAAA TCCTATCTTG TTGTCATTAT ATTTGCAACG	720
ATACATGAAA TTAGTCATGC AATAATTGCT AATAA	755

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CCAGAAAAAC CGTAGTGGAG CTCGTGGAAC AGTGAATTG ATTTTCCAAA AAGAATACAA	60
TAAATTTTCA AGTATCTCAA AGAGGGAGGC ATAAGATGTC AGATGCATTT ACAGATGTAG	120
CCAAGATGAA AAAAAACAAA GAAGAAATCA AGGCACATGA GGGACAAGTC GTAGAAATGA	180
CTTTGGAGAA TGGTCGTAAG CGCCAAAAA ATAGATTGGG TAAGCTAATT GAAGTTTATC	240
CATCTCTATT TATTGTGGAG TTTGGGGATG TGGAAAGAGA TAAACAAGTT AATGTTTACG	300
TTGAATCCTT TACTTACTCA GATATTCTTA CAGAAAAGAA TTTGATTCAT TATCTTGACT	360
AAAGTGAGAA ATTTTCTCAC TTTTCTTTT TTCTCCGAAT AATTAGGTG AAGGCAATCA	420
TCGCTTTATA TTATTTTTC AAGAGGAAGA ATGAAAATTT TACCGTTTAT AGCAAGAGGA	480
ACAAGTTATT ACTTGAAGAT GTCAGTTAAA AAGCTTGTTT CTTTTTTAGT AGTAGGATTG	540
ATGCTAGCAG CTGGTGATAG TGTCTATGCC TATTCCAGAG GAAATGGATC GATTGCGCGT	600
GGGGATGATT ATCCTGCTTA TTATAAAAA GGGAGCCAGG AGATTGATCA GTGGCGCATG	660
TATCTCGTC AGTGACTTC TTTGTAGCC TTTCGTTTGA GTAATGTCAA TGCTTTTGAA	720
ATTCCGGCAG CTTATGGAAA TGCGAATGAA TGGGGACATC GTGCTCGTCG GGAAGGTTAT	780
CGTGTAGATA ATACACCGAC GATTGGTTCC ATTACTTGGT CTAATGCAGG AACTTATGGT	840

1249

CATGTTGCCT GGGTGTCAAA TGTAATGGGA GATCAGATTG AGATTGAGGA ATATAACTAT	900
GGTTATACAG AATCCTATAA TAAACGAGTT ATAAAAGCAA ACACGATGAC AGGATTTATT	960
CATTTTAAAG ATTTGGATGG TGGCAGTGTT GGAATAGTC AATCCTCAAC TTCAACAGGC	1020
GGAATCATT ATTTTAAGAC CAAGTCTGCT ATTAAAAGT AACCTCTAGC TAGCGGAACT	1080
GTGATTGATT ACTATTATCC TGGGGAGAAG GTTCATTATG ATCAGATACT TGAAAAAGAC	1140
GGCTATAAGT GGTGAGTTA TACTGCCTAT AATGGAAGCT ATCGTTATGT TCAATTGGAG	1200
GCTGTGAATA AAAATCCTCT AGGTAATCT GTTCTTTCTT CAACAGGTGG AACTCATTAT	1260
TTTAAGACCA AGTCTGCTAT CAAAAGTAA CCCCTAGTTA GTGCAACTGT GATTGATTAC	1320
TATTATCCTG GAGAGAAGGT TCATTATGAT CAAATTCTCG AAAAAGACGG CTACAAGTGG	1380
TTGAGTTATA CGGCTTATAA CGGAAGTCGT CGCTATATAC AGCTAGAGGG AGTGACTTCT	1440
TCACAAAATT ATCAGAATCA ATCAGGAAAC ATCTCTAGCT ATG	1483

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1027 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

CCCGGAAAC AAGTTAAAGT TGAAGTTGGT CAAGCAGTTT ACGTTGAAAA ATTGAACGTT	60
GAAGCTGGTC AAGAAGTTAC TTTTAACGAA TTGTTCTTGT TGGTGGTGAA AACACTGTTG	120
TCGGAACTCC ACTTGTTGCT GGAGCTACTG TAGTTGGAAC TGTGAAAAA CAAGGAAAAC	180
AAAAGAAAGT GGTACTTAC AAGTACAAAC CTAAAAAGG TAGCCACCGT AAACAAGGTC	240
ACCGTCAACC ATATACAAA GTTGTCATCA ACGCAATCAA CGCTTAATTT TAAGGAGAAC	300
ACATGATACA GGCAGTCTTT GAGAGAGCCG AAGATGGCGA GCTGAGGAGT GCGGAAATTA	360
CTGGACACGC CGAGAGTGGC GAATACGGCT TAGATGTCGT GTGTGCATCG GTTCTACGC	420
TTGCCATTAA CTTTATCAAT TCTATTGAGA AATTTGCAGG CTATGAACCA ATCCTAGAAT	480
TAAACGAAGA TGAAGGTGGC TATCTGATGG TTGAAATACC AAAAGATCTT CCTTCACACC	540
AGAGAGAAAT GACCCAGTTA TTCTTTGAAT CATTTTCTT AGGTATGGCA AACTTATCGG	600
AGAACTATTC TGAGTTCCTC CAAACCAGAG TTATCACAGA AACTAACAC GGAGGAAAAC	660
ATTATGTTAA AAATGACTCT TAACAACCTG CAACTTTTCG CCCACAAAAA AGGTGGAGGT	720

1250

TCTACATCAA ACGGACGTGA TTCACAAGCA AAACGTCTTG GAGCTAAAGC AGCTGACGGA	780
CAAACGTGTA CAGGTGGATC AATCCTTTAC CGTCAACGTG GTACACACAT CTATCCAGGT	840
GTAAACCTTG GTCGTGGTGG AGATGATACT TTGTTGCTA AAGTTGAAGG CGTAGTACGC	900
TTTGAACGTA AAGGACGCGA TAAAAACAA GTGTCTGTTT ACCCAATCGC TAAATAAAAA	960
GGTCCATTGA ACCTTTTATC CCGAACCTTG AAATGTAGAG GTGAGGAAGC TAGAAACAGC	1020
TTAAAAAT	1027

## (2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1990 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CGGTTCAAAT GGTGCAGGTA AATCTACGTT AATTAATTCT ATTGTAGGTT TTCAAGAGAT	60
TTATTTAGGA GAAATAGAGT ATTGTGATAA AGATTGATA GTTAGTTCTC AACCTTTTGC	120
TCATTTAGGC TTTACTCCTC AAACCACAGT AATTGATTTT TATACTACTG TGAAGGACAA	180
TGTAATATTG GGGCTGAACC TTGCTGGAAA GTTTGGGAAA AATGCTGAGA AGTTGTGTCA	240
AATAGCCTTA GAAATGTTG GGTAGCTGA TAAAAAAAT AATTTGGTAG AACATTCTC	300
AGGTGGACAA CTGCAACGCG TCCAGATTGC TAGAGCAATA GCTCATAATC CAGATTTTTA	360
TATTTTAGAT GAACCTACCG TTGGTTTAGA TACTGAATCT GCCGAAAAAT TTTTAATGTA	420
TTTAAAGAT AAGAGTTTG AAGGAAAAAC TATTATCATA TCTTCACATG ACATAAATCT	480
ACTCGAAAAG TTTTGTAATA AAATACTTTT TTTACAAAAT GGCTCCATAT CATTTTTTGG	540
TGATATGCGT GACTTTGTAG ATAATTC AACAAATTA AATTTTTC AA TGCAGAATAG	600
AATTTCTAGA TATCAAAATG AATTTT TAGA AAATTT TAGA TTAAAGTTC ACATCGAAGA	660
TAATGATAGT TTTACAATAG AAGTCCCTAT AGAAGAAAAG ATCTTAGATG TTATCAATGA	720
GGTAGGAAAA GCATGTGAAA TTAAAACTT TTCAACAAGT AAATTAACCT TACAAGAAAG	780
TTATTTGCAA AGAATAGGAG GAGAAAAATG AAGGCTGATC AATTAAGGCA CAAATCGGAC	840
TTAGGTTTAA GAGGTCTAGC GATTATTGCT AAAAATGAGA TTATTGCTTT TTTTAGAAGT	900
AAAGGTTTAA TTATTTCTCA GTTCTACAA CCAATCTTAT ATGTTGTTTT TATAATAATA	960
GGATTAAATT CTTGATAAA GAACATTCAG TTTAATGATA TAAAAACCTC TTATGCAGAA	1020
TATACAATCA TTGGTGTTAT AGCTTTATTG ATAATCGGGC AGATGACTCA AGTTATTTAT	1080

1251

AGGGTGACAA TAGATAAAAA ATATGGGCTA CTGCTCTTA AGTTATGCAG TGGAGTTCCT	1140
CCTTTATATT ATATTTTAGG GATGAGTATC TATTCTATAT TAGGGTTGAT AGTTCAAGAA	1200
ATTATTATAT ATATAATTAC GTTAGCGTTT GAGATAAATA TCGCAATGGA TAGATTTT	1260
TATACAGTTT TGTATCTAT TGTGTTTTA TTATTTGGG ACTCCCTGC AATTTTACTT	1320
ACAATGTTTA TCAATGATTA CAGAAGACGT GATATTGTAA TACGTTTGT ACTAACACCG	1380
CTTGGTTTTA CAGCTCCTGT TTTCTACTTA ATAGATTCTG CTCCTAGTAT TGTGAGATGG	1440
ATTGGTCAGT TAAATCCCTT AACTTATCAA TTAATATTT TGAGAACTT TTATTTTAAA	1500
AATTCAACAA CTTTGAATT AGTTTCTTA TTGTTAACAT CATTACTTGT CCTATATCT	1560
GTATCTTTTA TTATACCAA GATAAAATTG ATACTGATAG AAAGATAAAA GTTGGGTCAT	1620
CCAACTTTTT TGTGCTCTCC CGAAAACCAC TAGCTATGCT AGTGGTTCCA TAGAGCTTTT	1680
AGCGTGGTAA CAAAAGAAC CTCCTAAAT GATAAGATAG AAGTGGTTC TCCGCCACTA	1740
CAACATATCA TACAGGAGGT ACCTCATGAG AGAGGATAAT CAAAGTTTAT CACATACCAC	1800
ATGGAATTGT AAATATCATA TTGTTTTGC ACCCAAATAT CGTCGTCAA TCATTTATGG	1860
CAGATACAAA GCTAGTATCG GAAGAAATCAT ACGTGACTTA TGTGAGCGTA AGGGTGTAAT	1920
AATCCATGAA CGGAATGCTT GTTCAGACCA TATTCATG CTATCAGTA TTCCTCCGAA	1980
ACTTAGTGTT	1990

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4766 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GAATATATT GCATATATTT CTAGCAATGA TCATGGCGAA TCTTGGTCTG CACCAACTTT	60
ATTACCTCCT ATAATGGGAC TTAATCGGAA TGCGCCATAT TTAGGTCCTG GACGTGGAAT	120
CATTGAAAGC TCAACTGGAC GTATTCTTAT TCCGTCTTAC ACTGGTAAAG AGTCTGCGTT	180
CATTTATAGT GACGATAATG GAGCATCTTG GAAAGTTAAA GTAGTGCCAC TTCCTTCTAG	240
TTGGTCAGCA GAAGCACAAT TTGTAGAATT GAGTCCAGGA GTAATTCAAG CATATATGCG	300
TACAAATAAT GGTAAAATTG CATATTTAAC AAGTAAAGAC GCAGGTACTA CTTGGAGTGC	360
ACCGGAATAT TTGAAATTTG TTTCAAATCC AAGTTATGGA ACACAATTAT CAATCATCAA	420

1252

TTATAGCCAA TTGATTGATG GTAAAAAGGC TGTCATTTTA AGTACTCCAA ACTCCACAAA	480
TGGTCGTAAA CACGGACAAA TTTGGATTGG TCTAATTAAT GATGATAATA CAATTGATTG	540
GCGTTATCAT CACGACGTTG ATTATAGTAA CTATGGATAC TCATATTCAA CATTGACAGA	600
GTTACCAAAT CATGAAATTG GATTGATGTT TGAAAAATTT GATTCATGGT CTCGTAATGA	660
ACTTCATATG AAAAATCTTG TACCATATAT AACATTTAAG ATTGAAGATC TGAAAAAGAA	720
TTAAAGCTGA AATTTGAAAA TATATAAAAA GAGGATAAAA ATTATGGTAA ATTACGGTAT	780
TGTTGGAGCT GGATATTTTG GAGCTGATTT AGCTCGCTCA ATGAACAAAA TTGAAGATGC	840
AAAAGTGGTT GCGGTATTTG ACCCAAATCA TGGAGAAGAA GTTGCTCAAG AGTTGGGATC	900
AGATGTTTGT GCAAGTTTAG ATGAACTTGT AGCACGTGAA GATATTGATT GTGTGATCGT	960
AGCTTCACCT AGCTACCTTC ACCGTGAACC AGTTGTGAAA GCTGCTCAAC ATGGCAAACA	1020
CGTATTTTGT GAAAAGCCAA TTGCATTGTC TTATGAAGAT TGTAAGCCA TGTTGACGC	1080
ATGTAAAGAA AATAATGTCA TCTTTATGGC TGGTCACATC ATGAACTTCT TTAACGGTGT	1140
ACACCATGCT AAAGAATTGA TTACTCAAGG TAAAATCGGT AAAGTTCTTT ATTGCCATGC	1200
TGCTCGTACA GGTGGGAAG AACAACAACC AACTGTATCA TGGAAGAAAC TTCGTTCTCA	1260
ATCTGGAGGA CATTTGTACC ACCATATTC AGAATTAGAT TGCATTCACT TTATCATGGG	1320
AGGACTTCCT GAAAAAGCGA CAATGGTAGG AGGCAATGTA TATCATAAAG GTGAAAACTT	1380
TGGTGATGAA GATGATATGC TCATTGTAAA CTTAGAATAC TCTGATGATC GTTATGCTGT	1440
TTTGGAATAT GGTAAATGCTT TCCGTTGGGG TGAACACTAC GTCTTGATT C AAGGAACTGA	1500
AGGAGCTATC AAAGTTGACT TGTCAATAC TGGCGGTACT CTTCGTGTTA AAGGTGAAGG	1560
AGAATCACAC TTCTTAGTTC ATGAACTCA AGAGGAAGAT GATGATCCGA CAGCTATCTA	1620
TACCGGTCGT GGTATGGATG GAGCAATTGC GTACGGTAAA CCAGGAGTAC GTTGCCCAT	1680
ATGGTTGCAA ACATGTATTG ATAAAGAAAT GGAATATCTA CATGACATCA TTAAAGGTGG	1740
AGAAATTACA GAAGAATTG AAAAAGTTCT CAATGGTGTA GCTGCTTTAG AATCAATCGC	1800
TACCGCTGAT GCATGTACTT TATCAGTTAA AGAAGATCGA AAAGTAAGTC TTTCAGAAAT	1860
CACAAATGCT TAACTTTTGT AAAACAGAAT AGTAAATTCT TGTCAATTATA TAATTTCTAA	1920
AGTTCTGTGA TACAATCAT TGAATAAAGA AATAGAGATG GGAAGTGGAT AATGCCCAGT	1980
CCCATTTTTT ATCAAAAAGT AATGAGATCA AAAATGTGGG AGTGTGAAA TGAAGATTAT	2040
AGGTATCGAT ATTGGCGGAA CAACAATTAA GGCAGATTTA TACGATGAGT TTGGAACGAG	2100
TTTGAATCAT TTCAAAGAGA TAGAAACAAT TATTGACTAT GATTTGGGAA CGAATCAGAT	2160
ATTAAATCAG GTCTGTGATT TAATTGGTGA GTATACTTTA AATCATTCAA TTGATGGTGT	2220

1253

TGGGATTTCC	ACTGCTGGAG	TTGTTAATGC	TAATACTGGA	GAAATCATCT	ATGCAGGCTA	2280
TACAATACCA	GGGTATATCG	GAGTAAACTT	TACTGCCGAA	ATAGAAAAAC	GTTTTGGGTT	2340
GTATACTTTT	GTGAAAAATG	ATGTTAATTG	TGCTGCATTA	GGTGAATTGT	GGAAGGGACA	2400
AGCCAAAGAT	AAGAAAAATG	TAGTAATGGT	TACTATTGGA	ACAGGTATAG	GAGGCAGTAT	2460
TATTGTCAAC	GGACAAATTG	TTAACGGATT	TAACATACT	GCTGGTGAAG	TAGGTTATAT	2520
TCCTGTAGGT	AATTCGGATT	GGCAAAGTAA	AGCCTCAACA	ACCGCATTGA	TTCATTTATA	2580
TCAAAAAAG	AGCTTGAAAA	CTAATCAAAC	TGGACGTACT	TTCTTCACTG	ATTTAAGATC	2640
TGGAGATAAA	GTGCTGAAG	AAACTTTTGA	AATTTTGTGA	GAAAACTAA	CAAAAGGTTT	2700
ATTAACGATT	TCTTATCTAC	TTAATCCAGA	AATTCTCATA	TTAGGAGGTG	GGATTCTGGA	2760
TAGTAAGGAT	ATTTTGTTAC	CTGAAATTC	AAGTTCTTTA	GCTAAAAATG	CAATGGATAA	2820
TAGGTTTTTA	CCTAAAAATC	TTGTGGCAGC	TACATTAGGA	AATGAAGCTG	GTCTATAGG	2880
AGCTGTAAAA	AATTTCTTAG	ATAGAATTTC	TAATAAATAG	TATGTAAGAT	AAGGAGGTGT	2940
CACAATGACT	AACTCTGTAT	TTTCGACAAT	GCAAGATATT	GAGAATGTTG	CAACCGATAT	3000
TATAAAATCA	TATGATAATG	AGATTTATAC	TTATAAAGCT	GTTTCCCAAG	AAGAATTGGA	3060
AAACTAGAA	AAAAGTTATG	ATGAAAAAAG	TCACGAAGAA	TTAGTTTCAA	TAGAAAGCAA	3120
TTTAGAAATG	AAACAACAGA	ACCTTATTGA	TGAGGTTAAT	AAAACAATCA	AGGAAAATGA	3180
TGCAAAATAT	CAGTATATTT	CATCAAGTAG	GAGAGCAGAA	TTTGTAGAAA	AAATTATTGG	3240
TAGGGTGGTA	GAAAAATATG	GCCATTAGTC	AGATGAAAAG	AATCTCTCTA	CTATTTTCTA	3300
AAAGTAGTCT	TGATGATGTT	TTAAAACTA	TTCAAGAACT	AGAGTCAGTG	CAGTTCCGTG	3360
ATTTAAAGGT	TCAGGATAAC	TGGTCAGAAG	CTCTAGAAAA	AGATGAAGTT	GTATTTCCAA	3420
CTATTCAAAT	TTTTCATACT	TCTAATTCCA	ATCATGGGGT	TATTGAGGGA	AATGATGCCT	3480
TGACTTATTT	GATGAATCAA	CAACAACATT	TAGAAGCAAC	TGTAGAGAAA	TTACAAGAAT	3540
ACCTACCGAA	AGAAAAACAG	TTTAAATTAT	TGCAGCAACC	TCCGATAACT	ACCTCTTATG	3600
AAGAATTAGA	GAAATTGGT	AAAGCTAATG	TTGCTGAGGG	TGTTCTTAAA	AAAGTGAATC	3660
ATCAAATTAA	CAGAGTTCAT	GAATTAGAAA	GACACATTCA	AAGTAATAAT	GAGGAAATAG	3720
AGCGATTAAT	AAAGTGGGAA	AAATTAGAAA	TTGTTCTCTG	GAATTTAGAA	CAATTTTCTT	3780
TCTGTAAAGG	AAAAGTCGGA	ACAATTCCAA	GGACTGAAGA	TAATCGCTTA	TACAATAGTC	3840
TTTTAGAAAA	CAATATTGAA	GTCAAGAAA	TATTTTCTAA	TGATAGAGAG	TACGGTGTGT	3900
TTGTTTTCTA	TCAGTCTAGT	TACTCTATAG	ATTTTGATGA	ATACTTATTT	GAACCATTTG	3960



1254

ATTATTCTAG AAAGGAATTA CCGAAGCAGC GAGTAGTAGA TTTAGATCAA GAAAACATGC	4020
AGTTAATAAC TGAAAAAGAG AATATTATCG CATCGTTGCA AGATTCAAAG AAATA'TTTGA	4080
TAGATTTACA ATGGCAAATA GACTATATTT TATCTATCTA TGCTCGTCAA ATCTCTAAGA	4140
ATAACTTTTT GTGCACTCCG CATCTAGTTG CATTAGAAGG ATGGATAGAA GAAACTCGTA	4200
TTTATATTT TATAAAAGTT ATGGATGAGC ATTTTGGACA TTCTATTTAT ATTTATGAAT	4260
CGGAAACATT GACGATAAT CAAGATGAAA TACCTATCAA ATTAACGAAT CATTCTTTAA	4320
TTGAACCATT TGAATTATTG ACAGAAATGT ATGCTCTGCC CAAATATTAT GAGAAAGATC	4380
CTACACCTGT ATTAGCACCA TTTTACTTTA CATTTTTTGG AATGATGGTT GCTGATTAG	4440
GCTATGGTTT ACTATTGTTT TTAGGAACAA TGTTAGCATT AAAAATTTT CATCTACCTT	4500
CAGCAACTAA GAGATTTTAA AAATTCTTTA ATATATTAGG GGTAGCCGTT GCAATTGGG	4560
GTGGAATCTA TGGCTCATTT TTTGGATATG AGTTGCCATT TCATCTGATA TCTACAACT	4620
CTGATGTCAT GACTATATTA GTAGTGTGAG TTGTGTTTGG GTTTATTACA GTATTTGCAG	4680
GTTTGTAGC TTCAGGACTA CAAAAAGTAA GAATGAATAA ATATGCAGAA GCATATAATT	4740
CAGGATTGTC GTGGTGTGTT ATTCTG	4766

## (2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2484 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

CCTTTTAGAA AAAATTAAAG AATACGACAC CATTATCATT CATCGTCATA TGAAACCAGA	60
CCCTGATGCC TTGGGAAGTC AGGTGGGATT GAAAGCCTTG CTGGAACATC ATTTCCCAGA	120
AAAAACCATC AAAGCCGTCG GTTTTGATGA ACCAACTCTT ACTTGGATGG CTGAGATGGA	180
TCTTGTGAA GATAGAGCCT ACCAAGGCGC ACTTGTATC GTCTGTGATA CAGCTAATAC	240
TGCTCGTATC GATGATAAGC GCTATAGTCA AGGTGATTTT CTCATTAAAGA TTGACCACCA	300
TCCAAATGAT GATGTATACG GTGACCTGTC TTGGGTCGAT ACTAGTTCAA GTAGCGCTAg	360
aGaTGATTAC CCTATTTGCC CAAACAACCC AACTAGCCTT GGCAGATCGC GATGCTGAGT	420
TGCTCTTTGC AGGAATTGTC GGTGATACAG GTCGCTTCCT CTACCTTCTT ACCACTGCAC	480
GGACTCTTCG CCTGGCTGCT TATTTGAGAG AACATAACTT TGACTTTGCG GCTCTCACTC	540
GCAAAATGGA CACTATGAGC TACAAAATTG CTAAACTGCA AGGCTACATC TACGACCATC	600

1255

TGGAAGTCGA	TGAAAATGGT	GCTGCTCGCG	TTATCCTGAG	TCAGAAAATC	TTGAAACAAT	660
ACAAATATAAC	CGATGCTGAA	ACTGCGGCCA	TTGTAGGTGC	ACCTGGACGC	ATTGACAGAG	720
TGAGTCTCTG	GGGAATTTTT	GTCGAACAGG	CTGATGGCCA	CTACCGAGTT	CGCTTACGCA	780
GTAAAGTCCA	TCCTATCAAT	GAAATTGCCA	AGGAGCATGA	TGGTGGAGGC	CACCCCTCTAG	840
CAAGTGGTGC	TAATTCCTAT	AGCCTAGAAG	AAAACGAAAT	CATCTACCAA	AAGTTAGAAG	900
ACTTGCTTAA	AAACTGATAA	AATACTTGCC	AACTTTTCA	GAATCTGATA	GACTAGTATA	960
GTAACAATCT	ATGGCTCGCA	AAGAGACCAT	GGCAGAAAGG	AAATATTGCA	AAATGAAAAT	1020
AGATATCCAT	CCAGAATATC	GCCCAGTTGT	CTTCATGGAC	ACAACTACTG	GTTACCAATT	1080
CCTTAGCGGT	TCAACAAAAC	GCTCTAACGA	AACAGTTGAG	TTTGAAGGCG	AACTTACCC	1140
ATTGATCCGT	GTGGAATTTT	CATCAGACTC	ACCCCATTC	TAACTGGAC	GTCAAAAGTT	1200
CACTCAAGCA	GATGGACGCG	TGGATCGTTT	CAACAAAAAA	TACGGTCTCA	AATAATGATA	1260
AGAGAACAGT	TTTGGCTGTT	CTTTTTTGT	TCTTGAAATC	AACTGCTGTT	TTCATGTTCC	1320
AGACTCATCT	GTAGTTTCCA	TTTCCATGCT	ACTAGGCAGG	AAGGAAATAG	CTGTTTCAAC	1380
ACGTCCATAA	TGAGCTATAC	TATTGTCACG	AACCACACTT	TCAATTGATGG	TCCAAGTGGA	1440
ATTCAATTTC	TTAAAAGCTT	CTCGGACTTT	TTCCAAATCT	TTGGAGGCAA	TGGCCTGCTC	1500
TAAGGTTTCA	AAACGAGGAC	TTATACTCAT	CTGCTTTCAA	AAAGCATTCT	AGTCCATCTC	1560
CGATTACCGA	TGGACTTTAT	CACCTCCTTC	TCCAGTCCTT	GTATGACATC	TTGAAGTTGA	1620
TTTATGACAT	CTTCCAAAGT	TGAAAAGGCT	TTATTCTTAA	ATCCACGTTT	ACGAATCTCT	1680
TTCCACACTT	GTTCAATGGG	TTCATCTCTG	GTGTGTATGG	AGGAATAAAG	GTAAAATCAA	1740
TATTAGTCGG	AATATTTAAG	GTAATTGATT	TATGCCATAT	AGCATTGTCC	ATAACGAGTA	1800
AAAGGATAAG	CTTGTGAAAG	CTCTTCTAAA	AAGGCGTTCA	TCCACACTCC	TTTTTATAAA	1860
CCTGAAATAA	GGCATCAATT	GTAACAAATT	CTCCTGCCTC	TGTAGCCTTC	AAATGACGGG	1920
CAAGAAAAGG	TTTCTCTTCC	TCAACTGTCA	TATATGCATG	GTTACGACCA	CCACGTGTTT	1980
CTTGAAGGAG	AGAGTCGAGT	CCGAACTCCT	CATATTTTTT	TACGTTTCGC	CAAAATCGTTG	2040
TTTGATTACA	GTCTAAAAGC	TCTATAATCT	CTTTATAAGA	TTTGCCCATC	AGACGAAATA	2100
TAGTAGATTG	AAACTAGAAT	AGTACACCTC	TACTTCTAAA	ACATTGTTAG	AAATCGATTT	2160
GTCTGTCTCT	TGTTTCATTT	TACTATAGAA	CGATTGGAAG	GCGTTTATAA	TATTTAGCTG	2220
TACGAGAGTC	TTTTAAAAGT	GTTTGTATGG	TTTGGATTTC	TTCTTTAGTT	GATTTCATAT	2280
TACTATTATA	TAATGCTTTT	TGATTTTAGT	CTGGTATAAA	TATTGCTTTC	CTCCAAAATG	2340

1256

GTCATAGTTT TACTGGCAA TCTAACATAT CACGGATAAA TTAACAAGTG ATTTCTGAAT	2400
TGCTAAACAT TTTCTTTTCT TATAGCATAC TTTAAGATT TGTCTTGAG AAAGATATTT	2460
CCAAGAAAAA CGTTCGTTTT TTGG	2484

## (2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1766 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

CTAGATATAG CTATAATTTT ATTTATAACA AGAGGATAGA AATGACCGAA TTAGAAAGAA	60
AAAATCGAAA AATTAGCTAA GAAATATTCT GATAACTTAA ACATCAAAGT TCAAGAGAGA	120
GTTCTGAAA TGGCAAATGA TAATAAGAGC CATTATTTGA TATACAGAGT TTTAGGTATT	180
TCATTTGAAG AAGGAGAAAA TATCGATTG TATCAAATA AAGGTCGTTT TTTATACAAA	240
TATGCTGGTT CATTTTGA GAAGCTGCA GTACTATGCT TTAACGAAAA ATTTGGTACA	300
GAAAAACTT AAAAAGTTAA CATTCCTAAT TCTGAAAGTA CAAAACCTAA GACTTTTGAA	360
ATTGATTGTT TACTCGGAGA AAAACACGCA TACGAAATAA AATGGTGGGA TGCAACTACA	420
GATGGAGACC ATATACTAA AGAACACACT AGAATAAAG TTATTCATAA CAAAGGATAT	480
ATACCAATTC GGTAAATGTT CTACTATCCA AATAGAACTC AAGCTATAAA AATTCAGCAA	540
ACTTTAGAAA CATTTGATAA CGGTATTGGA GGGAAATATT ATTATGGAGA TTCTGCCTGG	600
GAACATTTAA GAGCAGTGAC CGGTATTGAT TTACTTAGTA TTCTAACAGA TATTGCAAAAT	660
AAAAAACAG GGGTAAATC AAAATGACAG TATTAAAGG AGATAACTTA GAAATATTAA	720
AAACTATTGA ATCCTCAAGT ATTGATTAA TCTATATGGA CCCTCCTTTC TTTACACAGA	780
AAACCCAAAA ATTATCTAAT AACAAAAATA TTATGTATTC ATTCGAAGAT ACGTGGACTT	840
CGATTGAGGA TTACAAAGAA TTTTGTCTG TAAGATTAGA AGAATGCAA AGAGTGCTAA	900
AAAATAGTGG CAGTATTTT GTTCATTGTG ATAAAATTGC AAATCATCAT ATTAGATTAA	960
TTTTAGATAA TATCTTGGG GTAGATATGT TTCAAAGCGA AATTATATGG AACTATAAAC	1020
GGTGGTCTAA TTCAAAAAAG GGATTATTGA ACAATCATCA AAACATTTAC TTTTATTCAA	1080
AGTCAAAAGA TTTTAAATTT AATACAATTT TTACAGAGTA TTCTTCTACT ACAAATATCG	1140
ACCAAATACT AGTGAACGA AACGAGATG GAAACTCTAA AACTATATAT AAGGTTGATA	1200
ATAATGGTAA CTATATTCTA GCAAAAGAGA AAAATGGAGT TCCCCTTTCA GATGTTTGGA	1260

1257

ATATACCATT TCTTAATCCA AAAGCTAAAG AAAGAGTAGG TTATCCTACA CAAAAACCTA	1320
TTCTGTTATT AGAACAAATT ATAAAGATTG CTAAGTATAA AAATGATATA GTTTTAGACC	1380
CGTTCTGTGG AAGTGGAAGT ACTTTAGTAG CCTCCAAGAT TTTGAATAGA AATTATATGG	1440
GGATTGATTT ATCTGAGGAA GCTATCAATA TAACTCAGCA ACGTCTGGAA AATGTTATAA	1500
AAACAAGTTC AAATTTATTG AATAAAGGAA TCGAAGCATA TAGAACCAAA ACTGAGGAAG	1560
AGGAAAACAT TCTTAAATTA TTACAGGCAA AAATGTTTCA AAGAAATAAA GGAATTGATG	1620
GTGTTTACC TAAACATTTT CAAAAAAGC CGATACCTAT AAAAATTCAT AAAAATAATG	1680
AATGCTGAA TGAGAGTATC TCTTATTAC AGAATGCTAT AACTCCAAA AACTTGATT	1740
TTGGAGTAGT TATAAAAGT CATTCG	1766

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 748 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

CCGAAATCA AATTCAAACC ACGTCAACGT CGCCTTGCCG TACTCAAGTA CAGCCTGCGG	60
CTAGTTTCCT AGTTTGCTCT TTGATTTTCA TTGAGTATTA AACTAAATTA AATAATATTA	120
GCGCGGAGAA TTTCTAATTC TTCCTTGGTC AAGCGACGCC ATTCCCCTCG TTCTAGGTTT	180
TCATCTAATA CTAAAGTTCC CATAGTCAAT CGTTGCAAGT CCACCACTTC CTTGCCACAG	240
TAGCCACCA TACGCTTGAT CTGATGAAAC TTCCTTCTG CAATGGTCAC ACGGATTGG	300
CTTTGATTCT TTTCTGTATC TATGGATACA AGCTCCAGTA TAGCGGGTTC ACAGGTAAAG	360
TCTTTGAGAG GAATACCCTC AGCAAATGTC TCCACATCTT CTTGGGTCAT GATTCCTTC	420
ACTTGTGCCA GATAAGTCTT GTCCACATGA CGCTTGGGCG AAAGAAGAAC ATGAGCCAGC	480
TGACCATCAT TGGTCAAGAG CAAAAGACCA TCGGTGTCAA TATCCAAGCG TCCTACTGGG	540
AAAACCTCCT TACTCCGCGC CAAGTCATCC AACAAGTCCA GAACGGTTCT GTGCTTGGGA	600
TCCTCAGTCG CTGAGATAAC TCCTTTGGGC TTGTTTATCA TGAGTAGAC AACTCTTCA	660
TACTCCAACA CTTGCCCATC AAAGCGAATC TCATCTATTT TTTTATCAAT CTGCAATTTA	720
GCTGATTTT CTTTTTGACC ATTACAG	748

(2) INFORMATION FOR SEQ ID NO: 237:

1258

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1449 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

AAAAGATTAC ATTGCAACAA TTGAAAATTA TCCAAAGGAA GGCATTACCT TCCGTGATAT	60
TAGTCCTTTG ATGGCTGATG GAAATGCTTA TAGCTACGCT GTTCGTGAAA TCGTTCAGTA	120
TGCTACTGAC AAGAAAGTCG ACATGATCGT GGGACCTGAA GCTCGTGGAT TTATCGTGGG	180
TTGTCCAGTT GCCTTTGAGT TGGGAATTGG TTTTGC GCCT GTTCGTAAGC CAGGTAAATT	240
GCCACGCGAA GTTATTTCTG CTGACTATGA AAAAGAGTAC GGTGTCGATA CCTTGACTAT	300
GCACGCGGAT GCCATTAAGC CAGGTCAACG TGTCTTATT GTAGATGACC TTTTGGCGAC	360
AGGTGGAAC TTTAAGGCAA CTATCGAGAT GATTGAAAAA CTGCTGCTG TTATGGCAGG	420
TTGTGCCTTC CTGTGTGAAT TGGATGAATT GAACGGCCGT GAAAAAATTG GTGACTACGA	480
CTACAAAGTT CTATGCATT ATTAATGAAA ACAGTCCCTA GGGCTGTTT CTCTACACTA	540
GGATATAAAA ATAGACTATA ACTAGTTAGA GAAAAACTAT AATTGAAAAC TATATCTTCT	600
TGCAGTATAA TAAAAGGACT AAGTGTTTGA GATTGTCTT CAAACATATG CAATTATTC	660
TGAAAGAGTA CAGTTAGGAG AGGGTTATGC CGATTGCAAT TGATAAAAAA TTCCACGCTG	720
TTGAGATTTT ACGGACAGAG AATATCTTTG TCATGGATGA TCAACGTGCT GCCCACCAG	780
ATATCCGCTC TTGAAGATT TTAATTTTAA ATCTCATGCC ACAGAAAAATG GTCACAGAGA	840
CCCAGTTGTT GCGCCACTTG GCTAATACAC CCCTACAAC GGATATTGAT TTTCTCTATA	900
TGGAGAGCCA CCGTTCTAAA ACAACTCGTT CAGAGCACAT GGAGACCTTC TATAAACTT	960
TTCTTGAAGT CAAGGATGAG TATTTTGATG GGATGATCAT CACGGGTGCT CCAGTTGAGC	1020
ATTTACCATT TGAGGAAGTG GACTATTGGG AGGAATTTAG ACAGATGCTT GAGTGGTCTA	1080
AGACTCATGT CTATTCGACC CTTCATATCT GTTGGGGGGC TCAGGCTGGG CTTTATCTGC	1140
GCTATGGTGT AGAAAAATAC CAGATGGACA GTAAGCTATC AGGTATTTAT CCTCAGGACA	1200
CCCTAAAAGA GGGTCACCTT CTATTTAGAG GCTTTGATGA TAGCTATGTA TCCCCTCAT	1260
CACGGCACAC GGAGATTTCT AAGGAAGAGG TCTTAAACAA GACCAATCTC GAGATTTTAT	1320
CAGAAGGACC TCAGGTGGG GTTCTATTG TGGCCAGTCG TGATTACGA GAAATTTATA	1380
GTTTTGGTCA TTTGGAGTAT GACCGTGATA CTTTGGCAAA AGAGTATTTT CGAGATCGTG	1440
ATGCAGGTT	1449

1259

## (2) INFORMATION FOR SEQ ID NO: 238:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

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TACCCGCTTC TTTCAAGAGT TGGAGCAGGG CTTGTTTGCG ATCTTTTGTC ATAGTTCTTC      60
CTTTTAACGG CGTTTTCGAA GCACTTTATA GACAGCTAGT GCTAATGTAT AGTCTACCAT      120
ACTATGGATA ATTGTACCAA ATCCAAC TAG TACAAATAGA ACATAAAACA TATTTTCTAC      180
ATTGGTACCA GAAGTTGCGT AAAAAACGAC ACAGGCCAAT ACTTCAGCAA GGGCATGAAC      240
AACAGCCAAA ACAAAGTTGA AAATCCAGGA AGATTTTGGT TTATCTAGGG TATCGGGGAA      300
TTTTTGTAGG TAAAGAGCTC CTAAAGCACC AAAAGATATA TGGGAAAAAG CCCGAAAAAC      360
GATAACCATG GGATAGCCAG CCATCAAAAA TCCAAACTA GAGGCTAGGA TGACAAAAAC      420
TGCCATCAAG GCGACAAGA ACATGGCTAT AAAAATAGCG ATGTGGCTCC CCAAAGTATA      480
GGAAGCAGGT GGAATGACAA TCTTGAAAGG CATAACAATT GGAATCAAAA TCGCAATAGC      540
CGTTAAAAGG GCTGTCATTG TCATAAATTG TGTCTTTTTC CGTGTATTCA CAAGAATCTC      600
CTTTTAACT GCATATACAC TAGTATGGTA CAATAAACCA GACAATAAAG CAAGAATTTA      660
CTTGGGTTTA TAGATCATTT TTTAGTTAAA AGTTATAGTA GATTGAAACT AGAATAGTCC      720
ACCTCTACTT CTA AACATT GTTAGAAATC GATTGGCTG TCCTGATCGA TTTGTCCTGT      780
TCTTATTCG TTTTACTATA GTAAAGATTT CATTA AAAAG AACTGTATA GAGCAAAATC      840
TCCACCTTCA GGT TTGAAA GCGGAGATTG TTTnTTATTT TTTCCAGGGT TTGTAGTCGT      900
GGGA                                                                 904

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## (2) INFORMATION FOR SEQ ID NO: 239:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

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CACTCAACA TGACTTATAT CAAGACGGAT GGACTTCAAG ACGATGCCAA TCGCTTGAAT      60

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1260

CGTAACATTC AGTTTGGTGT TCGTGAATTT GCAATGGGAA CAATCTTGAA CGGGATGGCC	120
CTTCATGGTG GACtTCGTGT ATACGGTGGA ACTTTCTTCG TCTTCTCTGA CTATGTGAAG	180
GCAGCTGTCC GCTTGTcAGC CTTACAAGGA CTTCTGTGA CTTATGTCTT TACCCATGAT	240
TCAATCGCAG TTGGGGAAGA TGGTCCGACT CATGAACCAG TTGAGCATTt AGCAGGTCTT	300
CGTGCTATGC CAAATCTAAA TGTTTTCCGT CCAGCAGATG CGCGTGAAAC GCAAGCAGCT	360
TGGTACCTTG CAGTGACAAG TGAGAAAACA CCAACTGCCC TTGTCTTGAC ACGTCAAAAT	420
TTGACTGTTG AAGATGGAAC AGACTTCGAC AAGGTGCTA AAGGTGCTTA TGTGTATAT	480
GAAAATGCAG CCGACTTTGA TACCATCTTG ATTGCGACAG GTTCAGAGGT TAATCTTGCT	540
GTCTCAGCTG CTAAAGAATT GGCTAGTCAA GGCgAAAAAA TCCGCGTAGT CAGCATGCCA	600
TCTACAGATG TCTTTGATAA ACAAGATGCA GCTTACAAGG AAGAAATtCT TCCAAATGCA	660
GTCCGCCGTC GTGTTGCAGT CGAAATGGGT GCAAGTCAAA ACTGGTACAA ATATGTTGGT	720
CTCGATGGTG CCGTtCTAGG TATTGATACT TCGGAGCCTC TGCCCCAGCA CCAAAAGTAT	780
TGGCAGAATA TGGCTTtACT GTAGAAAATC TTGTAAAAGT TGTTCGAAAC TTGAAATAAT	840
CCTAAAAATC AGGGCGTAAG CTCTGGTTTT TCTTACCAGA AAAGTAAGGT ACAATCTTGT	900
AAAAGTAGCT GAAATTTGAT ATAGTAGTCC TATGTAAAAG ACAAAG	960

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2764 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

CGGGGCTCCc TAGTtCTTAG GGAGCTATTT TTGTTTTtTC AAGAAGTTAT CTtCTTGtAT	60
TTTtACTCA ATGAAAATCA AAGAGCAAGC TAGGAAACTA GCCGTAssTG CTCAAAACAC	120
TGTTTTGAGG TTGTAGATAA GACTGACAAA GTCAGGAACA CATATCTACG GCAAGGCGAC	180
GTtGACGCGG TTTGAAGAGA TTTTCGAAGA GTATTAGTTG TGAATCTGGT GCAGTCGTCC	240
CAGATTATtC TTATTAGTAG GGTCTTGTTT TCTATATCCC CTCGTAGTTA ACAAGACCTT	300
GAGCATTTTA GAAAGAGGAA TCTATGTCTA CGAAATATAT TTTTGTAAct GGTGGTGTGG	360
TATCGTCCAT TGGGAAAGGG ATtGTGGCAG CGAGTCTAGG CCGTCTCTTG AAAAATCGTG	420
GTCTCAAAGT AACCATTCAA AAGTTTGACC CTTATATCAA TATTGATCCG GGAACCATGA	480
GTCCTTACCA GCACGGGGAA GTTTTTGTGA CAGATGACGG AGCTGAGACA GATTtGGACT	540

1261

TGGGTCAC TA TGAACGTTTC ATCGATATCA ATCTCAACAA ATATTCCAAC GTGACAACTG	600
GGAAAAATTTA CAGTGAAGTT CTTCGTAAAG AACGCCGTGG AGAATACCTT GGGGCAACTG	660
TTCAACTCAT TCCTCATATC ACAGATGCTT TGAAAGAAAA AATCAAGCGT GCCGCTCTAA	720
CGACCGACTC TGATGTCATT ATCACAGAGG TTGGTGGAAC AGTAGGAGAT ATCGAGTCCT	780
TGCCATTCTC AGAGGCTCTT CGTCAGATGA AGGCAGATGT GGGTGCGGAT AATGTCATGT	840
ATATCCATAC AACCTTGCTT CCTTACCTCA AGGCTGCTGG TGAAATGAAA ACCAAACCAA	900
CCCAACACTC TGTCAAAGAA TTGCGTGGCT TGGGAATCCA ACCAAATATG TTGGTTATTC	960
GTACAGAAGA GCCAGCTGGT CAAGGAATTA AAAATAAACT GGCCCACTTC TGTGATGTGG	1020
CACCAGAAGC CGTTATCGAA TCGTTGGATG TTGAACACCT TTACCAAATT CCACTGAACT	1080
TGCAGGCACA AGGGATGGAC CAAATTGTTT GTGATCATTT GAAATTAGAC GCACCAGCAG	1140
CGGATATGAC AGAATGGTCA GCCATGGTGG ACAAGGTCAT GAACCTCAAG AAACAAGTTA	1200
AGATTTCCCT TGTGGTAAAG TATGTGGAGT TGCAAGATGC CTATATCTCA GTGGTCGAAG	1260
CCTTGAAACA CTCTGGCTAT GTCAATGATG CAGAAGTTAA AATCAATTGG GTCAATGCCA	1320
ATGATGTGAC AGCAGAGAAT GTAGCAGAAC TCTTGTCTGA TGC GGACGGG ATCATCGTAC	1380
CAGGTGGTTT TGGTCAACGT GGTACAGAAG GGAAAATCCA AGCCATCCGC TATGCGCGTG	1440
AAAAATGATGT TCCAATGTTG GGAGTCTGCT TGGGAATGCA GTTGACATGT ATCGAGTTTG	1500
CTCGTCACGT TTTAGGTCTT GAAGGTGCCA ATTCTGCAGA GCTTGACCA GAAACAAAAT	1560
ACCTTATCAT TGATATCATG CGTGATCAGA TTGATATTGA GGATATGGGT GGAACCTTC	1620
GTTTGGGACT TTATCCGTCT AAGTTGAAAC GTGGCTCTAA GGCTGCTGCT GCTTATCACA	1680
ATCAAGAAGT GGTGCAACGC CGTCACCGTC ACCGTATGA GTTTAATAAT GCCTTCCGTG	1740
AGCAGTTTGA GGCAGCAGGT TTTGTCTTTT CAGGAGTTTC TCCAGACAAT CGTTTGGTAG	1800
AAATCGTGGA AATTCCTGAA AATAAATTC TTTAGCTTG TCAGTATCAC CCTGAACTGT	1860
CAAGCCGTCC AAACCGACCA GAAGAACTCT AACTGCCTT TGTACTGCA GCAGTTGAGA	1920
ACAGCAATTA GCAAAATCAG AACCTTGAG AAAAATCTCA GAGGTTTTTT GCATACGATG	1980
ATATTGCAGT ATATCTGAGG TAGGGGTCCT CTGTATGTAC CTGCTACCGT TGAAATCAAT	2040
AGCGACTCCC TCTTGCCCTG TGCTAGTGAA TGGATTTATC AGTATATTGA AATGAAATAA	2100
AATTTGAACA AATTAAATTCG GAAAGCCAAA TCAATTCTTA GCAAAGTTTT AGGAACTGGA	2160
TTGTATAGTG AATTGAAATA AGATGTGAAC ATCTCTATCA GGAAAGTCAA ATTAATTTAT	2220
AGAAATATTT TAGCAGTCAA GATGTACTGT TATAGATTCA ATACATTATA CTTTTTTAAT	2280



1262

TTAATCCACT ATAGTAAAT GAAATAATA CAGGACAAAT CGATCAGGAC AGTCAAATCG	2340
ATTTCTAACA ATGTTT TAGA AATAGAGGTG TACTATTCTA GTTCAATAT ACTATCCCAA	2400
ATCATT CATA CCTCTCTCAA CTAGATGTAA CTTACAAAAC CCCTGACCTC ATGAGCCACT	2460
TTCTTCCTCC TCATGAGGTC AGTTTTACTT TCTGCTGTT CAGTATCGTT TTTCTCGCT	2520
AGATTTCCTC AAAAGGGCAG ACTCCTCCCT TGGTGCGTCA CACGATTTT TCATCTCGAC	2580
TGTTCTTTAA TGCATCATTA ACGACGCTTT TCTTCTAGGT GGTTCATAAG GAACAGGAAG	2640
ATTCAGGTTG ACTTTTCTAA TCCTAGAATA AAGTGCTGAA AACAAATCGG AATAGGCATA	2700
GAGACTAGAC AATTTGAGGA GCTGCTTGCG TCCTGTTCGA ACACATTTTC CCACCACGTG	2760
AAGA	2764

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1682 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

CCGTTTTTTT CATGTTCAG TACTACAACT TACGTTGTAG CGCCCTGCAC ATTGGTTTCGT	60
CTTGTTTCAGT TTTCAAAGGT CTTGTCACT TGCTTCTCTC AAGCGACAAC TATATTAGTA	120
TATCACAAC TCTTCGCTT GTCAACACTT TTTGAAGAT TTITAAGTTT TTTTAACTT	180
TTTTTCATCA AGTGGTCC TGACCAACATA CCATAGTCCG TACGGGATTC GAACCCGTGT	240
TACCGCCGTG AAAAGGCGGT GTCTTAACCC CTTGACCAAC GGACCTGAGT TGTTATTTTC	300
AACTCTTACT ATTATACAGT CTTTTCAAAC TTTGTCACT ACTTTTTTAA ACTTTTTTTA	360
TTAATTTTAC AACAGCTTCA GTTCGAGCTG TATGTGGGAA CATATCGACC GACTGGATAT	420
AATGAAGATC ATACACTTCT ACTAAGCGTA CCAAATCACG AGCCAAGGTC GAAACATTAC	480
AAGAAATATA AACCATTTT TCTGGTACAT AAGTAAGAAT AGTATCTAAT AACTTATCAT	540
CCAGACCTGT ACGTGGTGG TCAACAATCA AAGCATCTGC TCGGTAGCCT TCCTTGTAAC	600
AACGAGGAAT AATCTCTTCT GCCGTTCAG CTTCATAATG AGTATTGTCA AATCCCATT	660
TTTTAGCATT TCGCTTGGCA TCTTCAATAG CTTCTGGAAT AATATCCATA CCTCTGAGTG	720
TTTTTACTTT CTTTGCAAAG GCAAATCCAA TCGTTCCAAC TCCACAATAA GCGTCAATCA	780
AATGGTCTTC TTTATCAACA TCCAGCGCTT TTAATGCTTC GCTATAGAGG ACTTCTGTTT	840
GCTCAGGATT TACTTGATAA AAAGCTCGAG GGGATAGTGA AAATTCATAA TTGAGTACAC	900

1263

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CTTCTTGAAT ACTCTCTTGC CCCCAGATAA TCTCTGTCTT TTCACCATAT ATCTCACTGG      960
TTTTAGCTGT ATTTGTATTA ACAGCTACTG TCACAACCTC TGGGAAATCT TTAACCAACT      1020
CTTTTACCAA TTGAGTTAAA TTAAGCTGGC GGTTCGTAAC AATAATAATC TGAACCTGTC      1080
CGGTCTTTCT CGCGCGTCGG ACCATAATAG TACGGACACC TAGAACTTTT CTCTCATCCG      1140
TGATTGGAAT CTGGTGATAA GTAAGTAATT CTGCTAAGCG ATTAGCAATC ACTTGGGTTT      1200
CCTTATCTTG TACCAGGCAG TCTTTCAACT CTACTAAATA GTGAGAGTTT TGTGCATATA      1260
AGCCCGCCTT GACCTGATTT TTAATTTTTC GAGTCTGAAA TTGTAACCTA GCTCTGTAAT      1320
ATTTTGTTTC CTGCATTCCA ATAGTTGGAC GAATTTTATA ATTTTCATAT CCTGCAGGAG      1380
CAAATTTTTT CAGCGCTTGA TGAAGTAAGT CCGTCTTGAA CTCCAGCTGC TTATCATAAT      1440
GCAGGTGCAT GATTGGCAG CCTCCGCATT CATTATAAAT AGTACAAGAT GGCACAATTC      1500
GAAATTTAGA CTTCCTGTTG ACCTTCAGTA ATTTTGCTTC AACAAAGTTG CGTCTAATAG      1560
AAGTAATCTG ACAATAGATA TCTTCGCCTT TGAGAGCTCC TGGTACAAAG ACTAATGTTT      1620
TTTGGTAAAA GCCGATTCCC TCACCGTTAA TTCCCATGCG CTTGATTTT AATGGTATTT      1680
TT

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(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2524 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

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TTAACTTTGG TCAATTCTTT AAAGTCATCC TCTGTAAGCA TGTCTAACCA TTGATGTTTC      60
CCTTTATTGC TAAAATCACC AATCCGACT ACAGCTATAT CTAAATCTTT CCAACTATTT      120
TTCAAATTTT CAAAATATCT TGATTGCAAA ATACCATCTG CTAACAATTT ATTTTCTTGC      180
ACAATCGTTG CATTCATAAA TGTACACTCT CCATGAAATT TTCTAGACAT TTCATAAATC      240
AGTGTATTCA CATGGTATTT AGCGTGATG TGACTAGGAC CACCTGCTAG AGGATAGAAG      300
TGAACATTTT GGACACTTTT ACTGTGAATT AAATCTACTA AATTACTTAA ACTTTTCCCC      360
CAAGAAAAGC CAATTTTCAT ATTATCATCA ATTAGATTCC TAAGGACGCC TGCTGCAACT      420
TGAGAAATTC TTTAGATAA AATTGTTGGA GTATCATCAA ATTCATTGG AATAATTTCT      480
AAACTTTCCA AACTGTATTT TTCTTTTACA TAATTTTCCA ACTTAAACAT ATTGGTATCA      540

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1264

AAATCTCTA TTTCAATTTT AACAATTCCT ACATTCCTTG CTTCTGTTAA CATTCTACTA	600
ATAGAGGTTT TATAAATTC TAATTTTGCT GCTATTTGTG ACTGATTAA GTTTTCAATA	660
TAATACAGAT AAGCAATTTT AGAAAGCAGT TTATTCCTAT CTGATTCAT AACTTAACC	720
TCTTACGAAA CTACCTTAAC CATTATCCCA GCATTTTCTA ATGTAGCTAT ATTTTGTTTA	780
GAAAGTTTTT CGTCTGTTAT TACTTCATAG ACTTGACTTA AAGCAAATCT TCTTACTGTA	840
CCTCTTTTAT CAAATTACT TGAGTCAGTT AGGACAATGA CTTTATCCGA CACTGCTGAA	900
ATATATTGAA CTACCTCACT GCGCATTAAA TCTTTTCCGG TAAAGCCCAT CTCTTTATCG	960
TAACCATCTG TCCCAACAAA AGCTTGACAC ACATGAAAAG TCTGTATCAT TTCTTTTAAT	1020
AAAGGTCCTA CAGTCACCTG TGAATCTTTC TGAAACTCAC CACCAAGAAC AATAACACGA	1080
CATGAATCAT AAGCTCTCAC AAAATTTGCT ATAAAAACG AATTTGTTAC AATCGTAACA	1140
TTTCTTTTTT GCTTGCAAAT TTCCTCAGCA AGTAAAGCAC AGGTCGATCC AGATTCTATC	1200
ATTATGTTT CATTATCTGA CACCAATTTT ACTGCTTCCT GAACAATTTT TCTCTTAGTT	1260
TCATAATTAA TTGACAAACG TACATTTAAG TCATCTCCAC TATTTAATAC AGCATATCCA	1320
TGCTCTCTGT GTAATAAACC TTTTGACTCT AATTATCTA AATCTTTTCT AATCGTTACT	1380
TTCGATACAT TTAATTTTTC CGATAATGTA TTAACGTCGA TCTTTTCATA TTCTGATACT	1440
AATTTAATAA TTTGTTCCAA TCTTTTCATT TTACACCTCC GTTTTATCT ACCAAAATAA	1500
AAAGCAAAAA ACAACAAATT AACCTTTCGT TCGTAATTGT TTTTCTTTCG TTTTGTGAT	1560
AGGATAGACT TATGAAGAGG AGGAACTCTT ATGGAAATAT CTAAAGGAAT TATTTTAAAT	1620
ATTCAACACT TTTCAATTCA TGACGGTCCG GGTATTCGTA CAACTGTTTT TTTAAAAGGA	1680
TGTCCTCTGC GCTGTCCATG GTGTTCTAAT CCTGAATCTC AAAGAATGAA ACCTGAAAAA	1740
ATGAAAGATG CTCAACGAGA GAAATTCACC TTAGTCGGTG AAGAAAAGAC TGTAAGAAGAA	1800
ATTATTACAG AGGTATTAAA AGACAAAGAA TTTTACGAAG AATCCGGTGG AGGTTTAACT	1860
TTATCAGGAG GTGAAATATT TGCTCAGTTT GAATTTGCTA AAGCCATCTT AAAATCAGCT	1920
AAAGAACATC ACATACACAC TGCCATTGAA ACTACTGCCT TTGTTGATCA TGAAAAATTT	1980
ATTGATTTAA TTCAATATGT GGATTTTATC TACACAGACC TAAAACATTA TAATCTATA	2040
AAACATAAAA AAGTGACTGG GGTTTTAAAT CAAATGATTA TTA AAAACAT TCATTATGCT	2100
TTTTCACAAA ATAAAACTAT CGTTTAAAGA ATCCCAGTTA TTCCTAATTT TAACAATAGT	2160
TTAGAGGATG CAGAAAAATT CGTACTCTA TTTAACTCAT TAAATATCGA CCAAGTTCAA	2220
CTACTCCCTT TTCATCAATT TGGTGAAAAC AAATATCGTT TATTAAATCG GAAATATGAA	2280
ATGGATGGAA TCAACGCACT TCATCCwGAA GATCTTATTC ATTATCAAAA GGTATTTCTG	2340

1265

AACCACCATA TTAATTGTTA TTTCTAGTTT ATTCCTTGA AATGCTCTAG CTATTTGCAG	2400
ATAACAAGCA TCTATAATAC ATACTTAAC TTTCAAAAGG TTTAGCTAAA AAATTTTAGC	2460
CAAACCTTTT CTATTTTACC TTGCTCTAGA ATTTTAAAC TGCTATACTT ATCACAAAAA	2520
AACG	2524

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2359 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

CGTGCTGGG GGCTTGTGGT CAAAAGGAAA GTCAGACAGG AAAGGGGATG AAAATTGTGA	60
CCAGTTTTTA TCCTATCTAC GCTATGGTTA AGGAAGTATC TGGTGA CTG AATGATGTTT	120
GGATGATTCA GTCAAGTAGT GGTATTCACCT CCTTTGAACC TTCGGCAAAT GATAFCGCAG	180
CCATCTATGA TGCAGATGTC TTTGTTTACC ATTCTCATAC ACTCGAATCT TGGGCAGGAA	240
GTCTGGATCC AAATCTAAAA AAATCCAAAG TGAAGGTCTT AGAGGCTTCT GAGGGAATGA	300
CCTTGAACG TGTCCCTGGA CTAGAGGATG TGGAAGCAGG GGATGGAGTT GATGAAAAA	360
CGCTCTATGA CCCTCACACA TGGCTAGATC CTGAAAAAGC TGGAGAAGAA GCCCAAATTA	420
TCCGTGATAA ACTTTCAGAG GTGGATAGTG AGCATAAAGA GACTTATCAA AAAAAATGCGC	480
AAGCCTTTAT CAAAAAGCT CAGGAATTGA CTAAGAAATT CCAACCAAAA TTTGAAAAAG	540
CGACTCAGAA AACATTTGTA ACACAACATA CAGCCTTTTC TTATCTAGCG AAGAGATTG	600
GGCTTAATCA ACTTGGTATT GCAGGTATCT CTCCTGAACA AGAACCAAGT CCACGACAAC	660
TAACAGAAAT TCAGGAATTT GTTAAGACCT ATAAGGTAA AACGATTTT ACAGAAAGTA	720
ACGCTTCTTC AAAAGTAGCT GAAACTCTTG TCAAATCAAC AGGTGTGGGT CTTAAAACTC	780
TGAATCCTTT AGAGTCAGAC CCACAAAATG ACAAGACCTA TTTAGAAAAT CTTGAAGAAA	840
ATATGAGTAT TCTAGCAGAA GAATTAAAGT GAGGAAAGAA TGAAAATTAA TAAAAATAT	900
CTAGCAGGTT CAGTGGCAGT CCTTGCCCTA AGTGTGTTGTT CCTATGACCT TGCACGTTAC	960
CAAGCTGGTC AGGATAAGAA AGAGTCTAAT CGAGTTGCTT ATATAGATGG TGATCAGGCT	1020
GGTCAAAAGG CAGAAAACCT GACACCAGAT GAAGTCAGTA AGAGGGAGGG GATCAACGCC	1080
GAACAAATTG TTATCAAGAT TACGGATCAA GGTATGTGA CCTCTCATGG AGACCATTAT	1140

1266

CATTACTATA ATGGCAAGGT TCCTTATGAT GCCATCATCA GTGAAGAGCT CCTCATGAAA	1200
GATCCGAATT ATCAGTTGAA GGATTCAGAC ATTGTCAATG AAATCAAGGG TGGTTATGTC	1260
ATTAAGGTAA ACGGTAAATA CTATGTTTAC CTTAAGGATG CAGCTCATGC GGATAATATT	1320
CGGACAAAAG AAGAGATTAA ACGTCAGAAG CAGGAACGCA GTCATAATCA TAACTCAAGA	1380
GCAGATAATG CTGTTGCTGC AGCCAGAGCC CAAGGACGTT ATACAACGGA TGATGGGTAT	1440
ATCTTCAATG CATCTGATAT CATTGAGGAC ACGGTGATG CTTATATCGT TCCTCACGGC	1500
GACCATTACC ATTACATTCC TAAGAATGAG TTATCAGCTA GCGAGTTAGC TGCTGCAGAA	1560
GCCTATTGGA ATGGGAAGCA GGGATCTCGT CCTTCTTCAA GTTCTAGTTA TAATGCAAAT	1620
CCAGCTCAAC CAAGATTGTC AGAGAACCAC AATCTGACTG TCACTCCAAC TTATCATCAA	1680
AATCAAGGGG AAAACATTTT AAGCCTTTTA CGTGAATTGT ATGCTAAACC CTIATCAGAA	1740
CGCCATGTGG AATCTGATGG CCTTATTTTC GACCCAGCGC AAATCACAAG TCGAACC GCC	1800
AGAGGTGTAG CTGTCCCTCA TGGTAACCAT TACCACTTTA TCCCTTATGA ACAAATGTCT	1860
GAATTGGAAA AACGAATTGC TCGTATTATT CCCCTTCGTT ATCGTTCAA CCATTGGGTA	1920
CCAGATTCAA GACCAGAAGA ACCAAGTCCA CAACCGACTC CAGAACCTAG TCCAAGTCCG	1980
CAACCAGCTC CAAGCAATCC AATTGATGAG AAATTGGTCA AAGAAGCTGT TCGAAAAGTA	2040
GGCGATGGTT ATGTCTTTGA GGAGAATGGA GTTCTCGTT ATATCCCAGC CAAGGATCTT	2100
TCAGCAGAAA CAGCAGCAGG CATTGATAGC AACTGGCCA AGCAGGAAAG TTTATCTCAT	2160
AAGTAGGAA CTAAGAAAAC TGACCTCCCA TCTAGTGATC GAGAATTTTA CAATAAGGCT	2220
TATGACTTAC TAGCAAGAAT TCACCAAGAT TTAAGTGATA ATAAAGGTCG ACAAGTTGAT	2280
TTTGAGGCTT TGGATAACCT GTTGGAACGA CTCAAGGATG TCTCAAGTGA TAAAGTCAAG	2340
TTAGTGAAG ATATTCTTG	2359

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

TTCTTTCTGC TATAATCGTA TAAATACTT ACTTTAGGAG TTCTTATGAA AGTTGTAAAA	60
TTTGGAGGTA GTTCTCTTGC CTCTGCTAGT CAATTAGAAA AAGTTTAAAA CATCGTCAAA	120
AGCGATTGAG AGCGTCGTTT TGTAAGTCGTT TCTGCGCCTG GTAAACGCAA TGCTGAAGAT	180

1267

ACTAAGGTTA CGGATGCCCT GATTAAATAC TACCGCGACT ATGTTGCCGG TAACGATATT	240
AGCAAGAACC AAAGCTGGAT TATCGACCGC TATGCTGCTA TGGTTAGTGA ATTGGGACTA	300
AAACCAGCTG TGCTAGAAAA AATTTCCTAAA AGCATTTCACG CCTTGGCCAC TCTTCCTATT	360
GAAGAAAATG AATTTCTCTA CGATACTTTC CTAGCAGCCG GTGAAAATAA CAATGCCAAA	420
TTGATTGCTG CCTACTTTAA CCAAAATGGT ATCGATGCAC GCTATATGCA CCCTAGAGAA	480
GCTGGGATTG TGGTCACAAG TGAACCTGGT CACGCTCGCA TCATTCCATC AAGTTATGAC	540
AAGATTGAAG AATTGACAAA CACCAATGAA GTCCTTGTC A TCCCTGGTTT CTTTGGTGTC	600
ACTAAGGAAA ATCAAATCTG TACTTTCTCA CGTGGAGGTT CTGATATTAC AGGTTCTATC	660
ATTGCTGCTG GTGTCAAAGC TGACCTCTAT GAAAACCTTA CGGACGTTGA TGGTATCTTT	720
GCAGCCCACC CTGGTATTAT CCACCAACCA CACTCGATTC CTGAGTTGAC CTACCGTGAA	780
ATGCGCGAGT TGGCCTATGC AGGCTTCTCA GTCCTTCATG ACGAGGCTCT TCTTCCTGCC	840
TACCGTGGAA AAATTCCTCT GGTATCAAG AATACCAACA ACCCTGACCA TCCAGGTACT	900
CGTATCGTTC TAAACACAG TAATGATGAA TTTCCAGTTG TGGGAATTGC TGGTGACTCA	960
GGCTTTGTCA GCATTAACAT GTCGAAATAC CTCATGAACC GTGAGGTTGG ATTTGGCCGC	1020
AAGGTTCTGC AAATCCTGGA AGAACTTAAC AT	1052

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 855 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

CCCTCGAAAA CTAAGCCGAT GAAGTCAGAA CACTTCAATC CTGTTCTGTA CTGGTGGGAA	60
AATCGTGAAG AGATTCTGGA AGGTAAGTTC TACAAATCTA AATCATTTAC ACCTAGTGAA	120
TTGGCTGAGT TGAATTATAA TTTAGACCAG TGTGACTTTC CAAAAGAGGA AGAGGAAATC	180
TTAAATCCCT TTGAGTTGAT TCAGAATTAT CAAGCGGAAA GAGCAACTTT AAATCATAAG	240
ATTGATAATG TATTAGCTGA TATTTTGCAG TTGTTGGAGG ACAAATAATG ACACCAGAAC	300
AACTTAAAGC AAGTATTCTC CAAAGAGCGA TGGAAAGGAA ATTAGTGCCG CAAAATCCCA	360
ATGACGAACC TGCAAGTGAA TTATTAAAGA GAATTAAGC TGAAAAAGAA AAAGTTATCA	420
GTGAAGGAAA AATCAAACGA GATAAAAAGG AAAGTGAATG ATTTCTGTTG GATGATGGGA	480

1268  
AACATTATGG GAACTTTGCT GATGGAAGCA CTCAAGAAAT TGATGTTTCCT TATGATATTC 540  
CTGATACTTG GGAGTGGGTG AGGATAAAAT CAATTTATTG GAATTTTGGG CAAAAAAGC 600  
CAGAGAAATC CTTTAGGTAT ATAGATACGT CTAGTATTGA TAGAAAAAG AACATAATCA 660  
ACTACAAAA TCTACAATAT CTTTCACCTG AACAAGCGCC TTCCCGTGCT AGAAAATTAG 720  
TTTCGCAGAA TAGTGCTTA TTTTCAACAG TTAGACCATA TCTAAAAAT ATTGCTGTAG 780  
TTAGAGAACT TAAAGAGTAT TTGATAGCTA GTACAGCATT TAATGTTTGG GGATACTTTA 840  
CTTAACGAAA CATAT 855

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 660 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

TTTAGGAAGG CTATCCGTAA TTTTACAAAG GATTTAGATA TTACAGAGGA ACATTTAGAT 60  
ATTATCAAAA GAGAGATGTT TGGCGAATTT TTCAGTAGCA TGAACCTCTT TGAATTTATT 120  
GCAACGCAAT ATGATGCTTT TGAAATGGT GAGATAATTT TTGATTTGCC GAAAATTTTA 180  
CAGGAAATTA CTTTAGAGGA TGTCCTTGAT GCTGGACATC ATTTAATAGA TGATGGTGAC 240  
ATAGTTGATT TTACAATATT CCCATCGTAG TAACCTATTA TAATAGACAC TAGAAAGAAG 300  
GGATGACAAG TATGAGAAAA AAAACAATTG GAGAGGTTTT ACGATTAGCT AGAATCAATC 360  
AGGGATTGAG TTTAGATGAA TTGCAGAAAA AGACAGAAAT CCAGTTAGAT ATGTTGGAAG 420  
CAATGGAAGC AGACGATTTT GATCAACTTC CAAGTCCTTT TTACACGCGT TCTTTCTTGA 480  
AAAAATATGC ATGGGCTGTT GAGTTAGATG ACCAAATTGT TTTGGATGCT TATGATTTCTG 540  
GGAGTATGAT TACTTATGAG GAAGTAGATG TTGATGAAGA TGAGTTGACA GGTCCTAGAC 600  
GTTCAAGTAA GAAAAAGAAG AAAAAACAT CATTTTACC TTTATTTTAT TTTATCCTGG 660

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1805 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

1269

CCGGTTGCAC AGGATCGTGC ATAGTCAACT CTTCAAGTAT AGCATATCTC CTATTTTCTT	60
ACAAGTAATA ACACCTAAAA TGAAGCTTTT TCTTTTACTT TTTTCTGCCA AGAGGCAAAA	120
AGCATGCTGA GGTAAAAAAC GCTCATCATA ATAGGAACAC CAAGAATGGT CTTTTCATGA	180
TAGAAAATCG TCAAAATAGG TGAAGAGACA ACGCCAAGGA CAAAACACT AAGCAGGCTA	240
ACAAATATGA ATCCTTCACG CAAAAAAGGA GTGTGCTTGG TTCGGAAATA ATCTCCAAAA	300
GCCAGCATGG TCCGTTTGAT ATTCCCTGTC ATAAAAGCGT TATTATAGGC AATACCCGAC	360
ACTTCTCCAA AAGCAGTTGT CACCAGTCCC ATACAGAAGG CCAAGGGCGG CACTAGATAG	420
ATATTATCCA CAGTTTGCGG CACAAAAGCA ATAATGATTG ATAAGATTGC CAAGGGAATC	480
AAGGACAGAA TAGGTTTTTT CACAATTCTC AATTTTTCCT TATAAATCGT TAATAAAAAAG	540
ACTCCCATCA TAAACGCTAG CAAGGTGAGA ACCTTGTCCT TAACATCCGA AACATTATTT	600
TTAATTAATT CTACTGAAAG AAAGACAACA TTTCCAGTTT GTCCAGCTAC AAGGGTATTC	660
CCGCGAACAA TAAAAGTGTA AGCATCCACA TATCCAGCAC AAAACGTCAA AAAAAGTGCT	720
AACCTTTTAG ACTGACGTGA TATTTTCTT ATAGGTAATA ACCTCATTTT ACCTCCCAT	780
GTATTTTCTC TTAGAAATAT TGTACCATT TCTTTCTAAA AAATCGTAGG CTACCATTTA	840
GATTTTACTA TTAGCATAAA AATAATAATA GACAACTATT TATCCAAAA TAGATAGATG	900
TAACATGTTT GCAACAAAG CATACGAACC TTTAGTAAAA TCATTTCCT GAAACTAGAA	960
TAGAGCCCTC TTAGCAAAAA TCATTATTTT AATTTATTTT TAATCACTCC TTGACATAAA	1020
TAATCTCAC CAATAAAAGA CTATGTCTTA AAAAAATGGT ATAATAAAAT CAATACTTGG	1080
GCTTGATGGC TATGCTACTA ATAACAATTA GGAGAGAAAA TCAGGCACCT GTTAACAACA	1140
AGGATTATCC CCTTGAGATG AAAGGAACTT TAGAAATCTT ATGATGAACA TGCAAAACAT	1200
GATGCGTCAA GCACAAAAAC TTCAAAAAACA AATGGAACAA AGCCAAGCTG AACTTGCTGC	1260
TATGCAATTT GTTGCAAAAT CTGCTCAAGA TCTTGTCCTA GCGACCTTAA CTGGCGATAA	1320
GAAAGTTGTC AGCATTGATT TCAATCCAGC TGTCGTTGAC CCAGAGGACC TTGAGACTCT	1380
TTCTGATATG ACCGTTCAAG CCATCAACTC TGCTCTTGAA CAAATCGATG AACTACCAA	1440
GAAAAAAGT GGTGCTTTTC CTGGGAAATT ACCTTTCTAA AAACAAGGAG CTAGAACAAT	1500
GCTTGTCGAT AACAAAGGCT AAGAAAGGTG CAAAAATGAC TCTATAATAT TTGTAGTGGG	1560
TAAATCCCCT ATGGATATTA TGGAGCCTAT TTTTGTGTAG AAAAAAGTCC CATATGACCT	1620
ATAATGAAAA GCGACAAAAC AACTCATTAG AAAGAATCAT ATGGAACAAT TACATTTTAT	1680
CACAAAATTA CTAGACATTA AAGACCCTAA TATCCAGATT TTAGACATCG TCAATAAGGA	1740



1270

TACACACAAG GwAATCATCG CCAAAC TGGr CTATGAAGCT CCATCTTGTC CTGAGTGCGG 1800

AAGTC 1805

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2516 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

CTGCATCTAG TTTGTTTCTC CCTACAGTTT TAGCTAGACA GATTGGAGAT TATGATTAA	60
CGTCGCCGCG TTGGGGTTCG GATACAATA GTGAGCTTGA GAAAGAAAAC TCCTCTGCTG	120
GAATTAATAA TAATGACAGC ACTGGTGGCG GTAAAAGGTT AAATACCTCT ATTCGTAGCG	180
CCTATAGTGG GTCAGATATT ACCCCGCTAT ATTCATTGGG GTCTGGCTCT AGGATTGTCA	240
TGTACTATAA TGGAGGTGGT GACAATTATA TTGGTTCTGG TACTAGATTA GCTATGGCGC	300
CACAATTTGG AAATCATGTA AGAATTCATA CTTCAGGTTC TTGGAATCCA GATTCTTATT	360
AACTTACTTG TCAGAGTAAG CCTTAAAGAT GGTGATTGT GGGGTAGCA TGAAAAAGA	420
ATGCTACACC CTATTTTAT TATAAGGAGG AGTAAGGATG GAATTTTCA TTTGTAATCT	480
TGTACGAGTC GTTCAATCAC CTCGATTTTA TATGCTTTA TTTTGGACCC TTCTTTGCAT	540
GAGTTTAGGA AATTCCTTG CTTTCAATGG TATTTATAAA ATTGAAGGT TATCGATTTT	600
TTTPGCCGCT TCTTCTATT C GAGGATTTT ACCGATTAGC CTAGTAGCTG CACTTATCTG	660
TACACTGCCC TATTCTAGTC AGATAATAGA GGATGCTGAG AGTCATTTTC TAACAGCACA	720
ATTGTGTCGA ATTTCTAAAA AGAAGTATCT GGCTATTGTG GGTAGTACTG TAATTATTTC	780
TTCTTTTCTA GTCTTTTTC TCCCCTATTT ATTATTATTA GGAATTAATC TTTTAGTGAC	840
TCCTTATCAG GAAATTTATA TTGGAGATTA TAGTGGTGCC TTAAGAAGAT TATTTGATTC	900
CAATCAGTTT CTCTATAGTC TTGTAACGAC TCTCTGGTAT GGAGTTTGGG GCGCTGTGTT	960
CTCTATTTT GGACTAGCTA GTGCTTTGCT AGTGAAGAAA AAAATAGGAG CTATTTTCAT	1020
CCCAGTTGCC TATATGATGG TTGGTGGTAT TTTTGGGCT ATTTTAGGGC TATCTTACTT	1080
AGAACCTGTG ACAACGCTAG CTTTGGGATA TCAGAAAGAT ATCAGTCTTT CCTTAGTTAG	1140
TGCTCATCTT GCTTTTATTT TATTTGTTAG TTGTTTGTT GTTTATGGTA CATTTTCTCT	1200
ACATTCAGAG GACTATGTAT AATGAAACAA TTTGTTCAAT TTTATAAAAA AGATTCTTCA	1260
GCAGTATTGG TTTATTTTAT ATTACTGCTA TCCTGTGTTT TATCTAGTAC AGTATATTTA	1320

1271

TTGCGCtGTC GCCAATATTC AATCCATCCA AATGTATTAG AATGGATCTT AGTTTTACTT	1380
CAAGATATGA CGACTGGAGT ATATTGCTTT CCGTTCACAT ATATATTGTT CTTTTTTTAT	1440
TTGATGAATA ACTATTTTAA TAGGTTGGAG TGTCGCATTC GTCTGAAATC AATTAAGCAC	1500
TTTACCAGTT TTAGTTTCAA ATTAGCAGCT CTTAGTACGG GGATTTGGAC GGCGACTTTA	1560
TTTTTATTGA TTTTCTAAT TGCATTTAGT AATGGTTTTA GCTTCTCTTT GGAGATAAAG	1620
GAGGTTGATT TTTTAAGAGA ATTTTATGGT ATAAGTATTG CAAACAATGC TAGTTTCTTT	1680
ATAGGATTTT TTTTCTCTTA TATAGCATAC TATTCTTTT TATCCTTACT TACTATTAGC	1740
AGTTTTTCTT GGTTTAAAAA ATCAAACATG AGCTTAGTAT TTCTGTTTAC TTTTTTATTT	1800
GTAGAATCCT TATTCTGGAT TTATCAGTTG GACAATGGGA TAATTGGATT ATGCCAATT	1860
TTTCAGTATA TGGTAAATTC CAATCCGTAT GCATTGATTT ATTGGCTTAC ATTACTATCT	1920
ATCATAATTC CATTGACTGT ATTTTCTGTT CATAGAACT GGAGGAGAGT GTAAAAGTTG	1980
GAAATGGGAA AGTTAAGTAG TCACATGTGG AGGTGAATC AGATAATCTA TACCAAGTAC	2040
TTTTGGGGTT ATGTTCTTTT TTGGATATTG ATTTGTTTAG GATTATGGTA TTGGTTAGAA	2100
GGAAATGATA GACTTGTTAT AGAAATTTTA AAAGGGCCTA ATCTGAGTCA AACTCTTTT	2160
TTAGTCTTAT CTATATGGTT GCTTCATTGG TTTATTATTC ATACATTTT TCTAGCAGTT	2220
GTATATCGTA GAAGAGCATC CGATTTCTTT ATGGAAGTGA TTCGATTTTC TTCTATTAAG	2280
CTCTGGATTA GGTATCAGAT TTGGACCTGT TTTCTTTATG GACTCATTTT AATCATGGTA	2340
AAAGTTCTAG TGATTCAATT TATGTTACAG TTACCAAAT GGGATATAGG AGTTTGTTT	2400
ATAGTTGATT CTTTGAATGC TTGTGTGTTA GTCTTGTTTT GCTTTATGTT ATACGCACTA	2460
CGAGCGAATG TACAAATGAA CTTTGCTTGC GTTAGTTTCT TTTTACTCAT GATTGG	2516

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1364 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

CGGTGTTTTT TTGTAAATTT TCTAGCACTT GTATGGTAAA ATAGATACAG GTGTTCATTA	60
AACTAGACTA AAAACCTATT TAAGCAGGCA AAATGAAGAA ATACCAACAA TTATTTAAGC	120
AAATCCAAGA AACCATTCAA AACGAGACTT ACGCTGTCGG AGATTCCTT CCTAGCGAGC	180

1272

ACGACCTTAT GGAGCAATAT CAAGTGAGTC GTGATACCGT CCGAAAGcCC TGTCTCTCCT	240
CCAAGAGGAA GGATTGATCA AAAAGATAAG AGGGCAAGGT TCTCAAGTCG TCAAAGAAGA	300
AACCGTCAAT TTCCCTGTAT CCAACCTAAC CAGCTACCAA GAACTAGTTA AAGAACTTGG	360
ACTGCGCTCT AAAACCAACG TGGTCAGTCT GGACAAGATT ATTATTGATA AAAAATCCTC	420
ACTGATAACC GGTTTCCCAG AGTTTCGGAT GGTTTGGAAG GTGGTCCGCC AGCGTGTGGT	480
GGATGATCTG GTATCCGTTT TGGATACGGA CTATCTGGAT ATGGAACCTCA TCCCAAATCT	540
CACTCGCCAA ATTGCTGAGC AGTCTATCTA TTCTTATATA GAAAAATGGCC TCAAACCTCT	600
TATTGATTAT GCTCAGAAGG AAATCACCAT TGACCACTCA AGCGACCGAG ACAAGATTCT	660
CATGGACATT GGCAAAGACC CTTATGTCGT TTCGATTAAA TCAAAAGTCT ATCTCCAAGA	720
CGGACGCCAA TTTCAGTTTA CCGAAAGTCG CCATAAGTTA GAGAAATTTA GATTTGTAGA	780
TTTTGCAAAA CGCAAGAAAT AAAAGACTGA GACACCAGAT CTCAGCCTTT TTCGGCTCTA	840
TAATATTTGT AGTGGGTAAC CCCCCTATGG ATATTATGGA GCCTATTTTG TGTAGAAAAA	900
AAGTCCCAT A TGACCTATAA TGAAAAGCGA CAAAACAACCT CATTAGAAAG ATTCATATGG	960
AACAATTACA TTTTATCACA AACTGCTCG ATATTAAAGA CCCAAACATC AAGATTCTAG	1020
ACATCATCAA TATGGATACC CACAAAGAAA TTATCGCTAA GCTGGATTAT GAGGCTCCAT	1080
CTTGCCCTGA TTGTGGAAGT CTAATGAAGA AATATGACTT TCAAAAACCG TCTAAGATCC	1140
CTTACCTCGA AACAACTGGT ATGCCTACTA GAATTCCTCT TAGAAAGCGT CGTTTCAAGT	1200
GCTATCATTG TTCTAAAATG ATGGTCGCTG AACTTCTAT CGTCAAGAAG AATCATCAAA	1260
TTCTCTGTAT TATCAACCAA AAAATTGCGC AAAAGTTGAT TGAGAAGATT TCTATGACCG	1320
ATATTGCTCA TCAGCTGGCC ATTTCAACTT CAACTGTCAT TCGG	1364

## (2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1227 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CCATGAAGAC CGCTTGGAAT TGGAATGGCA CAAGTCTTTG TTGAATGGTC TATTCCTATT	60
GACAATCGGT GGAGGAATTG GACAATCTCG TATGGCCATG TTCCTACTTC GCAAGAGACA	120
CATCGGAGAA GTGCAAAACAA GTGTTTGGCC TCAAGAAGTC CGCGATACTT ACGAAAATAT	180
TTTGTAGAGA ATCGAACCGC AAGGTTGGT TTTCTTTCTC TTTTGTCTA TAATTGGTA	240

1273

TAATAAACAG TATGAAAATC GTATCAGGAA TCTATGGGGG ACGTCCCCTC AAGACACTAG	300
AAGGCAAGAC GACAAGACCT ACTTCGGATA AGGTTAGGGG AGCCATTTTT AACATGATTG	360
GTCCCTACTT TGAAGTGGGA CGAGTCTTGG ACCTTTATGC AGGTAGTGGT GGTATTATCTA	420
TCGAAGCAGT ATCGCGTGGC ATGTCCAGTG CTGTTTGGT GGAGCGAGAC CGTAAGCTCA	480
GACCATCGTG GCTGAAAATA TCCAGATGAC CAAGGAAGTT GGAAAATTC AACTCCTCAA	540
GATGGATGCA GAAAGGGCAT TGGAACAGGT ATCTGGGGAA TTGACCTCG TTTCTTAGA	600
CCCTCCCTAT GCCAAGGAAC AAATCGTAGC AGATATTGAA AAAATGGCTG AGAGAGAGCT	660
TTTTTCTGAA GATGTTATGG TTGTGTGCGA GACGGATAAA GCCGTTGAAC TTCCAGAAGA	720
AATTGCCTGT CTGGGTATCT GGAAGGAAAA GATTTATGGA ATTAGTAAGG TGACAGTCTA	780
TGTCAGATAA GATTGGCTTA TTCACAGGCT CATTTGATCC GATGACAAAT GGGCATCTGG	840
ATATCATTTGA ACGGGCGAGC AGACTTTTTG ATAAGCTTTA TGTGGGTATT TTTTTAATC	900
CCCACAAACA AGGATTCTC CCTCTGAAA ATCGTAAACG GGGGTTAGAA AAGGCTGTGA	960
AACATTTGGG AAATGTTAAA GTCGTGTCTT CTCATGATAA ATTGGTGGTC GATGTCGCAA	1020
AAAGACTGGG GGCTACTTGC CTAGTGCAG GTTTGAGAAA TGCGTCGGAT TTGCAATATG	1080
AAGCCAGTTT TGATTACTAC AATCATCAGC TGTCTTCTGA TATAGAGACT ATTTATTAC	1140
ATAGTCGACC TGAACATCTC TATATCAGTT CATCAGGCGT TAGAGAGCTT TTGAAGTTG	1200
GTCAGGATAT TGCCTGCTAT GTTCCCG	1227

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3652 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

CCGGTCAAGT TAAAAACGCT ATTTCTTCCC ATTTTATTTA TTTTITAGGA GTGGTAACGT	60
ATCAAAATAG CCCAAGCGTT CTCACCCGTG TGAGTTTGAA TAATGGAACC CGTTTCCAAA	120
ACAGAAATTG GCTTTTCAAC ATAAGCTTGT AAGCTTCTT TCATCTCTTT TGCCCAATCA	180
TCACTACCAG AATATGAAAT TCCAATCTCT GCTACAGCAC GTTCAGAAAG CGATGTTATC	240
AACTCATCTA ACCATTTTTT AAATGTTTTA GTTCCACGAC CTTTAACCAT TGGCTGCAAT	300
TCATGGTCTT TCATTTGCAT GACAGCACGG ATATTGAGAA GAGAGCTCAA CAAGCCAGTT	360

1274

ACACGGCTAA TTCGTCCACC TTTGACAAGA TTTTCCAAAG TTGAAACACC AATATAAAGC	420
TCTGTATGGT TTTTAACCTC TTTTACATGA GATAAAATTG CCTCCATATC TTTACCTTCT	480
TGAGCTAACT TCGCAGCCTC AACAACTTGG AATTTTCAGGG CTGGTTCAGT GAAGGAACTA	540
TCAACAACAG TCACATCTGC AGTAGATAGG CTAGCACCTT GCGTGTCTGC TTCTACCGTA	600
CCCGAAAGAG CATGGGACAT ATGAATAGCA AGAATCTGGC CACCATCTTT GCATAGGTCT	660
TCAAAAATCT CAGCAAAGAC ACCTACAGGT GGCTGACTTG TTTTCGGAAG ATTCTTACTT	720
TCTTGCATCA ACTGAAGAAA TTTACCTTCT TCTTTCAAAT CCGCATCAGA ATAAACAACA	780
TTATCAATCA TTACAGATAA TGGAAACAATT GTAATATCTA ATTGCTTTAC TAGTTCAGGT	840
TCAATAGTAA CAGATGAATC GGTTACAATC TTAATTTTTC TCATAGTATC AATCTTTCTA	900
TTTTAGGATT CAGATTGGTT TCCTTACTTC TAATTATATC AAAAAAAGA TTAAAAATCC	960
TAATGGAGTC AATCAAATTT TCCGTAAAT TTGATATAAT CAACTTATAA GAAAAGAGGT	1020
GTCTATGAT TAAAAAATTT TACCCCATTT TTACCATTTT ACTAGGTGCT GCTATTTATG	1080
CTTTTGGACT GACTTATTTT GTAGTTCCCC ATCATCTCTT TGAAGGAGGG GCGACAGGCA	1140
TTACCTCAT CACCTTTTAT CTTTTTAAAA TCCCTGTTC CCTCATGAAC CTGCTGATTA	1200
ATATCCCCCT TTTCATCCTA GCTTGAAGA TTTTGGAGC CAAATCCCTC TATTCTAGTT	1260
TACTAGGAAC CTTAGCTTTG TCCGGCTGGT TAGCTTTTTT TGAGCATATT CCCCTTCATA	1320
TTGATCTTCA AGGTGATTTA CTAATCACAG CCCTTATAGC GGAATCCTA TTGGGAATTG	1380
GCCTTGAAT TATTTTAAAT GCTGGAGTA CAACGGCGG AACTGATATT CTAGCTCGTA	1440
TTCTCAACAA ATACACTCAT ATATCCATAG GAAACTGCT CTTTATCTTA GATTTTGTGA	1500
TTCTCATGTT GATTCCTCCTA ATCTTCAAGG ATTTGAGATT GGTTCCTAC ACGCTTTGT	1560
TTGATTTTAT TGTTTCTCGT GTTATTGATT TGATTGGTGA AGGAGGATAT GCCGGCAAAG	1620
GCTTTATGAT TATCACAAAA CGTCCTGACC AACTTGCTAA GGCGATTAAT GATGACCTCG	1680
GAAGAGGTGT TACTTTTATT TCTGGTCAAG GCTACTATAG TAAAGAAAAT TTGAAAATCA	1740
TCTACTGTAT TGTCGGAAGA AATGAAATTG TGAAAACGAA GGAAATGATT CATCGAATCG	1800
ATCCTCAAGC CTTTATAACT ATTACAGAAG CCCATGAAAT CCTAGGAGAA GGCTTCACCT	1860
TTGAAAAAGA ATAAAAAGAG GTAATGTCGT GACCTCAAAA GTTAGACTAA ATCATCTATC	1920
TTTTGGGTTA CAGACAACCT CTTTTTATT TTATTACTC AAGCTCTTAA GACCAATTCC	1980
GAGTTACTTC TTCATCAGCC TTTAACTGAT CCACTAATTG GTCAACTGAG TCAAATTGG	2040
TCATATCTCG AATGCGATCA AGCCAATAAA CCATGACGGT TTCCCATAA ATATCTTGAT	2100
TAAATCAAA AATATTGACT TCAAAACGTG CTTCTTCTCC ATCAAAGGTC ACATTTTTC	2160

1275

CGACACTAGC CATAGCACGA TACTTCTGTC TTTGAATCTC AACATCAACA ACATAAACGC	2220
CATCTGCTGG CATATAAGTA CGGTCTAAAA GCACTAAATT CGCTGTCGGA TAACCAATTG	2280
TACGACCACG AGCATTACCA TGAACCACCA TACCTCTTGA TGAAGCGGT GCCCCAAAA	2340
GTTTTCCCTGC TTCTTTTACA TTTCATCTA AAATAGCTTG ACGGATACGA GTTGAACATA	2400
TCTTTCCTTT CTCATCTTCT ACAGGTGGAA CAATGATAAC TTCTCCATCA AAGTAATTCT	2460
TTAAATCTTC TGCTGTTTTT TTGTCAGAAC CAAATGTATA ATCAAAACCT GCAACAATAA	2520
TTTTGGCATT CATAGCCTTG ATATAAGTTG CAAAGAATTC TTGTGCAGTG AGACTAGCGA	2580
ATTGACTACT AAAATCAAGG AGATATAATT CTTCTACACC TTCGCGCTTT AATTTCTTTT	2640
CACGTTCAAG AGGGTTCAAA ATATGCAAAA ACAAACTCTGG ATGATAAGGC TCTAAAGCGA	2700
TCTTTGGAGA TTCATTAAAG GTCATAACGA CGATAGGCAA CAAATCCTTT CTCGCAGCCT	2760
TGTTGGCAAC ACGAAATAAT TCTTGATGCC CCTTATGTAT GCCATCAAAA TAGCCGAGAA	2820
CAACGACTGA ATCAGATGGT GTGCCAATAT CTTTTTGTT TTTTATAGGA ATAGTAATAA	2880
TCATAAAATA ATTATATCAT AGCGATAGCT ATTTCTGGAA CAGAAAATCT GAAATGTGT	2940
TTTTTTCACA TGAAGGTAC CTGTTTTCAA AAAGCACTTT ATTCTATCGT TGCTTAACTA	3000
TGAACCTTGC AATATTCTTC TCAAAAACCT GTAGGACATC TTCAAAATTT TGCAAGGAGT	3060
GATTAGACTT GTTCGGTAAC CATAAAGTGT CATACTATGC TTATGTATGA AAAAGCAATG	3120
CAACTAACTC CTGAGAACTT TAAATTACTA ATTGGTGCCG AAAAGGTAGA ATTTAGAATC	3180
GAGGTACACC TATGGCTGTA AAATTTACAA AATGAGACAA CTTGGGCAAG ATGTTTGAAG	3240
AATTTCTTAA ACTCCCTGAT TTGAAGCAAG TCACCTTCCC TAATGACAAA GAAAAAGCC	3300
AAAACAGCAA AGAAAACTA GATGACTGCT TTCCAACAAC TCCCCTCTAG TGTGCTTCAG	3360
ACTGGGCTAT TTTTCTCTCC ATCTGTTAGC TTGGATTCTC AGACCGTTTC AGCTAAAGAA	3420
TATCTTTTCC CTTATCAGAA GGAACGGCTC AAGCCATTCA GACAAGTGAA GGGACGACAA	3480
GCCAATATTT GAAACCAGAT AGCAGTTCTT ATAGTCAATT GAAATAAAAT CTGAAGAAAT	3540
CGAGTAGGAA ACTCATATCA ATGTTTAACA GTGTTCTATT CCAGATTCAT ACTCAATGAW	3600
AATTAAAGTG CAAACTAGGA AGTTAGCCGC AGGTGATACT TTGGGTACGG CA	3652

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 743 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GTACCGTGGT GCCAAAGTAC AGCAAGGTG GCTTTTGGAC AAACAATACC AATCTTGGTT	60
TTACATCAAA GAAATGGAA ACTATGCTGA TAAAGAATGG ATTTTCGAGA ATGGTCACTA	120
TTATTATCTA AAATCCGGTG GCTACATGGC AGCCAATGAA TGGATTGGG ATAAGGAATC	180
TTGGTTTTAT CTCAAATTG ATGGGAAAT GGCTGAAAA GAATGGGTCT ACGATTCTCA	240
TAGTCAAGCT TGGTACTACT TCAAATCCGG TGGTTACATG ACAGCCAATG AATGGATTG	300
GGATAAGGAA TCTTGGTTTT ATCTCAAATC TGATGGGAAA ATAGCTGAAA AAGAATGGGT	360
CTACGATTCT CATAGTCAAG CTTGGTACTA CTTCAAATCC GGTGGTTACA TGACAGCCAA	420
TGAATGGATT TGGGATAAGG AATCTTGGTT TTACCTCAA TCTGATGGGA AAATAGCTGA	480
AAAAGAATGG GTCTACGATT CTCATAGTCA AGCTTGGTAC TACTTCAAAT CTGGTGGCTA	540
CATGGCGAAA AATGAGACAG TAGATGGTTA TCAGCTTGGG AGCGATGGTA AATGGCTTGG	600
AGGAAAAACT ACAAATGAAA ATGCTGCTTA CTATCAAGTA GTGCCTGTTA CAGCCAATGT	660
TTATGATTCA GATGGTGAAG AGCTTTCCTA TATATCGCAA AGTAGTGTCT TATGGCTAGA	720
TAAGGATAGA AAAAGTGATG ACA	743

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4010 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

TTTTGGTTGA TGATACGAGG GATTTGGTGA TTCTTCTTGA CGATAGAAGT TTCAGCGACC	60
ATCATTTTTG AACAGTGATA GCACTTGAAT CGACGCTTTC TAAGGAGAAT TCTAGTAGGC	120
ATACCAGTCG TTTCAAGATA AGGAATTTTA GAAGGTTTTT GAAAGTCATA TTCTTCAAT	180
TGGTTCCGC ACTCAGGGCA AGATGGGGCG TCGTAGTCCA GTTTGGCGAT GATTCCTTG	240
TGTGTATCCT TATTGATGAT GTCTAAAATC TGGATATTAG GGTCTTTAAT GTCTAGTAAT	300
TTTGTGATAA AATGTAATTG TTCCATATGA TTCTTTCTAA TGAGTTGTTT TGTCGCTTTT	360
CATTATAGGT CATATGGGAC TTTTTTCTA CAATAAATA GGCTCCATAA TATCTATAGT	420
GGATTTACCC ACTACAAATA TTATAGAACC GAATTAATTT AATTAGAGAG CCAACTTTCT	480
AATATAGTAA TCGCGTCATA ACAAGGTATC TATCATTCAT GGAGTTCCTC CTGTATACTA	540

1277

TTAGTAAAGT AAAACTATTG GAGGATATTT TAATGCCACA ACCTATTGTT CCTGTAGAGA	600
TTCCACAATC TCGTCGTTTT GATTCTAAAA AGAGAAATGA TATTCTGCTT AAAATTCGTA	660
TTGGCAAGCT TGAAGTAAGT TTTTTCAT CTCTCAATCT CGAAATGGTA GAACAGCTTT	720
TGGATAAAGT GTTGCTCTAT GACAATTCAT CTATCTAGCC TAGGGCAGGT CTATCTCGTA	780
TGTGGGAAAA CGGATATGAG GCAAGGCATT GATTCAATTGG CTTATCTGGT TAAAACCCAC	840
TTTGAATTAG ATCCTTTCTC CGGTCAAGTT TTTCTCTTTT GTGGTGGACG TAAAGACCGC	900
TTTAAAGCCC TTTACTGGGA TGGTCAAGGA TTTTGGCTAC TATATAAAG CTTTGAGAAC	960
GGAAAACTGA CTTGGCCCAG TACAGAAAAG GATGTCAAAG CTCTCACACC TGAACAAGTA	1020
GATTGGCTTA TGAAGGGCTT TTCTATCACT CCAAAAATAA ATTTATCAGA AAGTCGTGAT	1080
TTCTATTGAA ATGAGGACTT TCTTTTGTAGT TATAATAAAG TTAGGAAATA AGGAGAGGAA	1140
GCCCATGGAA GAAGATTGAA AATCATTCAA CAACAGAGTG CTACAATTGA TAGTCTCACC	1200
AATGAAGCTG CCCTTCTTCG TGAACAAGTG GCTTATCTAA CGAAAAGCT CTATGGAAAA	1260
TCCTCTGAGA AAAGTGTTTG CCCATCTGGA CAACTCAGTC TTTTGAAGA GGAACAAAAT	1320
ATGGAAGAAG ACTCTGACTT ACCCAGTTGA AAGAGAAGAA ATCACCTATA AACGTAAGAA	1380
AGCTAAAGGG AAACGTCAAG CTCTTCTTGC CCAATTTGAT TCAGAAGAAG TTCATCATCA	1440
AGTAGAAGAG AGCATTTGCC CTGATTGTCA GGGAGATCTA AAAGAGATTG GAGCAACCCCT	1500
TCAACGACAA GAATTAGTCT TTATTCTGTC GCAATTAAAA CGAATAGATC ATATCCAACA	1560
CGCTTATAAG TGCCAAGCAT GCAGTGATAA AAATCCGAGT GATAAAATCG TGAAAGCTCC	1620
TATTCCTAAA GCCCCTTTGG CGCATAGCCT TGGCTCAGCT TCTATTATCG CTCACCCAT	1680
CCATCAGAAG TTTAATCTGA AGGTACCCAA TTATCGCCAA GAAGAAGATT GGGCTAAGAT	1740
GGGTTTACCA ATCACACGTA AGGAAATTGC TAATTGGCAT ATCAAGGCGA GTCAATACTA	1800
TTTGAGAGCCC CTTTATAATC TTTTACGAGA AAAGTTGTTA GAACAAGCTC TTCTTCATGC	1860
GGATGAAACC TCTTATCGGG TTCTAGAGAG TGATAGTCAG TTGCCTTACT ATTGGACTTT	1920
TTTGCTGGG AAAGCTGAGA ATCAAGCAAT CACGCTGTAC CACCATGATC AGCGTCGGAG	1980
TGGTTTAGTA GTACAAGAAT TCCTAGGAGA TTATTCTGGC TAIGTTCATT GTGACATGTT	2040
GCGGCAGTAA CTTAGGACTT TAGTCCTCTA GTTCTGCCTA TGCGATAGCA GTCCAAGGTT	2100
TAGGAGTAAG GCGACGCTAA CCTTGGTAAA CTGCCAACAG CTAGAAGCTT ATCGTCAACT	2160
GGAAGAAGCT GCACTTGTG GATGTTGGGC GCATGTGAGA AGGAAGTTTT TTGAAGTGCC	2220
CCCCAAGCAA GCAGATAAAT CATCCTTAGG AGCTAAAGGT TTAGCTTATT GTGATCAGTT	2280



1278

ATTTTCCTTG GAAAGAGACT GGGAGGCTTT GCCAGCTGAT GAACGACTAC AGAAACGTCA	2340
AGAACATCTC CAGCCCCTAA TGGAGACTT CTTTGCTTGG TGCCGCCGTC AGTCAGTTTT	2400
AGCAGGTTCA AAAC TAGGAA GGGCAATTGA ATACAGCCTC AAGTATGAAG AAACCTTTAA	2460
GACTATTTTG AAAGACGGAC ATCTGGTCCT TTCCAATAAT CTAGCTGAAC GCGCCATTAA	2520
ATCATTTGGTT ATGGGACGGA GTAAAAGAGT CCAGTGGACT CTTT TAGCCT GAGCTCAGTT	2580
TAAAAAAGCG AGGGTGGTTA TTTTCTCAA GTTTTGAAG AGCTAAAGCA AGAGCTATTG	2640
TTATGAGCTT GTTGAAACA GCTAAACGTC ATCAATTATA GTGCGTTGAA TCTATAACAG	2700
TACGCATCGA CTGCTAAAC ATTTCTATAA ATCAATTTTC CTTTCCTAAT CGATTGTTC	2760
ATATCTTATT TCAATCCATT ATAAATAGCG AGAAATATCT ATCCTATCTT CTAGAATGTC	2820
TTCCAAACGA GGAACTCTC GTAAACAAAG AGGTTTTAGA GGCCTATTTA CCGTGGACTA	2880
AAGTTGTACA AGAAAAGTGC AAATAAGAAA TCTCCAGATT AGGAACTATC CGTGAGTTCT	2940
CTAGTCTGGA GATTTTTCAA TAGACTTCGT TATTGGACGG TTACAATTTA TTATATGAAA	3000
ATCCCATATT ATTCTCCAAT TCTATATTTT ACCTTTCTAA ATGTATAGAT TAACTACCTA	3060
ATTATAGCAT ATAACGCAGA TTCCTTTCAA TCGTATGATT TACTGCATTA AATTAAGTAA	3120
AAAAATAAAG GCAGTCCGAA GACTGCCGAT ATTTATCTCT CATCTCTTTA ATTATGGTAA	3180
GTAAATAAAT AATTTCCCTA AAGATATGGA AATTATTAAT ACTATAAATA CATATTATAA	3240
AGTTTATAAA TACTGTAAA ATCCTGAAGT TAATTTTCTA ATAAATATCA ATATGTGTAA	3300
GTATCTTTTA AATTTT TAGA CAATTTACTA GTTCTATAGA CATGTTTAAC AGACTCTATT	3360
TTACAATTCA AAAATTTT CAT CTGCCACTTC ATTTAAAAAT TCTATATCAT GGGAAACAAT	3420
AAAAATTATT TTATCCATGG TTTTATACTT ATTAATCAGT TCAGATATTT TTATCATATT	3480
GGAATAATCC ATACCACTTG AAGGTTCCGTC AAAAAAGACA AATGGAGAAT TCTTGCACAT	3540
AACAGATGCT ATTGCAAGCC TTTGCTTTTG CCCTCCTGAT AAAC TCATCG GATGCCTTTT	3600
AATAAATTCG TCCAGGCATA AATCTTTTAA CCCAAATCAT TCATACCTCT CTCAACTAGA	3660
TGTAACCTAC AAAACCCCTG ACCTCATGAG CCACTTTCTT CCTCCTCATG AGGTCAGTTT	3720
TACTTTCTGC TGTTCAGTA TCGTTTTC TCGCTAGATT TCCTCAAAAG GGCAGACTCC	3780
TCCCTTGTT CGTCACACGA TTTTTCATC TCGACTGTTC TTTAATGCAT CATTAACGAC	3840
GCTTTTCTTC TAGGTGGTTC ATAAGGAACA GGAAGATTCA GGTGACTTT TCTAATCCTA	3900
GAATAAAGTG CTGAAACAA TTCGGAATAG GCATAGAGAC TAGACAATTT GAGGAGCTGC	3960
TTGCGTCCTG TTCGAACACA TTTTCCCACC ACGTGAAGAA AAAGATGGCG	4010

(2) INFORMATION FOR SEQ ID NO: 254:

1279

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2789 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

ATGCATCCGT TTGTCAAGCC TAAATTGTAA TTTTTCCTCA TTTAAACAG AAAAACCCAG	60
GAAAATGACA TAAAAATATC ATTCCTAGGC CTATTTATGC TATTCTCTC TGAAAAATAT	120
GAGTATTCAG TCGGTCAAAT GAAGCTGAAC GAACTCATTT TCCCTCGCCT AATTCAATGA	180
TTGATGACA TTGTTGGGCT ACATAAGCAT CGTGGGTCAC GATAATGACT GTTTTCCCCT	240
CTCGATTAT CTCTAAGAGA AACTTCAAGA CCAATCTCT ATTTTCAGGA TCCAGAGAAC	300
CTGTCGGTTC ATCGGCTAAA ATCAGCTGGC TGGGTTTAA GATGGCTCTA GCAACTGCAA	360
TTCGTTGTTG TCGCCCCCA GACAACTCGG AGACCCCTTG ATGCAAAGTA GCTGATAAAC	420
CTACTCTCTC TAAATCTCT TCCACCTTTT TGAGCTTGTC TTTCTTAGGC AATTTCACAT	480
ATTTTCAGGC CACATGAGAT TGTACTCGAC CGTTTCATCA TCAATCAGGG CAAAATTTTG	540
AAACAGATAA GAGATATGTT CACGGATTAT TGTGTCGAC TTAGCAGAAT TAACCGCTAG	600
ATTTGTCTGA CAAAAATCT CATACCGTCC GCTATAATCA CCATCTATCA AACCCAATAA	660
ATTTAACAAG GTCGACTTCC CACTACCACT CTTACCAACA ATAGCTACCA AATCCCCCTG	720
ATCAATCCTG AGAGATAAGT TATCCAAAAT CACTTTTCCC CCAATGGTTT TGGTAATATT	780
TTTCAACTCA ATCATAAGAT GCCCCTTTC AATAACTCTA CTAGACTTCT TTTCTCCATC	840
CTAGAAGCTA AGCCTAGCAC AAATAGTATA TCCAGACATG TAAACCTGC AAACACTAGA	900
AGTGGTAAGA ACGCATGGGC AAAGAAAATC AAGACTAGAA GAGGGAAACT ATAGCCCAGC	960
AAGAGCAGAA CGAGGAGAGG ACGGTAGCGA TCGACCAGTT TCCACCCCAT AAATTTCTTG	1020
GTAATGATAT CCCTGCGCTT CAATAAGAAA GTTGTACTA GTAAGAAGTA GGAAATCATC	1080
ATGCTAAGGA GACCAAACA AGCAAAGAGT AGGTTAAAT TCCGAACAGC ATCTCGATAA	1140
GAATCCACTT TCTCTTGTG AATGGCTTGA ATAGATGAAA ATTTTAAATA ATTTCCATCT	1200
GACAATTTCT CAACTAACTC TGTAATCTCT TTTTGATGTT GAACCGTATT TTCAATTTTA	1260
ATCGGATTAT TTAAGCCAGT TGTTGACAGG GAGGCTTTCT CATCCACAT CATATCAGAA	1320
TCATTGACCA AGCTAATAAT TGGATTGGAG AGATTTTCCT TTCGCTTATC ACTATATGGG	1380
AAAAATGACC AATCTCCTTC ATAATAGGCA ATCTCGACAT CCATCTCCTC TATCGTTCGT	1440

1280

TTTTGCTGCT	CTTCATACTT	CATCGAATGA	AAGGCAATTA	ACTTCCCCAA	GAGCTGATTT	1500
TTATCTTCTT	CACCTTTCGT	ACTTGCTGGC	ATCAAAATAA	CTTTTTTAAT	ACCGGTATTT	1560
GGTAGCTTGA	ATCCCTTGCT	CTTTAGAAAA	TTGCGATTGG	CATAGTAAAC	ATCCACCGTA	1620
TCTGTAACT	GATATTGCTG	AATCTGTTCT	GATTGGACAA	AATTTTTTAC	AGGAAGACTG	1680
CTACTCTGCA	CATAGCCCGC	CTGCGTTTTT	TCTACCAAAT	CCTGATAAAA	TCGATAGAAA	1740
TAATCTGTAG	ATTTCCCTGA	CCCTGCTAGC	TCTTCTTGCC	ACAGATTATC	ATTGAGTTTG	1800
AAGGTTTCTA	AGGTCAGGTA	ATTACCTTGA	CTTACCCACT	GTTGCTGATA	AGCAAGTTCT	1860
TTGTTTTCTT	GTTCTAAACT	TCTGCCCACC	CCAATCAGTA	AGGCCGTCAG	TAAAATAGTT	1920
GTCCCTATTT	TCATCACATA	ATTGAAGATA	AGACCAAATT	TGAAAGATGA	AAAACCTTTC	1980
AGCAGAGAGC	TGATTGTCAT	TTTTTGATT	AAGAGGTAAG	TCAACCAACT	GATAAAGAGA	2040
TAAAGCTGCA	ACAGCAAAAA	ATGAGACAAC	CACAGCATAG	GAAACAAATC	TTTTGGCTTA	2100
TAATCAAGCA	AGAAAAACAC	GCCTAGATTG	ATCACAAGAG	CCCCACCTAG	GAGGAGGTAA	2160
AGGTTGCCTT	TTACAACATC	AGCTAAAACA	GCCCTATCTT	GAAAACCAAG	TAATTTTGT	2220
ACCCCAACTC	TTTTCATCTC	CATCATCGGT	TGATACACTG	TCACTAACAC	AAGAAGCAAA	2280
ATAGCCAAGA	CAAAAAACAAT	GGCAGATAAA	AGCAAAATCTC	CATTATAGAC	TTCCACTGCA	2340
CTTTTGTAGG	TCGGCTCTAG	CAAGGTAGCC	TGGTCTATCT	TGAAAAAATC	GCTCCATTTT	2400
TGTACAATCC	TATCCTTGTC	CATCTCTTGT	GTAGAAGTTA	TCGTATAGCG	ACCATTTAAA	2460
CTACGAGATG	TATCCTTGAT	ATAGGTTTGA	AAAGTCATAA	GCTGAATAGG	TTTGGCTTTT	2520
AGAAAGGTCG	GAATCGTACC	AAGTTTATTG	GAAATTTCTT	TATTACTATA	GACTCCTTCA	2580
CCATCTGTGG	TAAATCAAG	AGAAGAAATC	CCAAACTCTT	GGTAGGGGAA	GGTATCTTTA	2640
TCAAAAACAC	CAGACTTGAC	CACCTCATCA	CCACTGTCTG	TTTTGATGAT	GGAGACTTTA	2700
TACTCCTTTG	ATACATCCTC	AAAAAATCGA	AGAACAGACG	CTGCAGGTTC	GTAAATATCT	2760
TTCAAATACA	AATCCAAAGA	ATCTACAGG				2789

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2495 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

CTGCGAATTT	TATTAAAGAT	AATGTGTTAA	TTACAGCGGC	TCACAACTAC	TACAGACATG	60
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1281

ACTATGGGAA AGAAGCGGAT GATATTTATG TTCTTCCGGC TGTAGTCCA AGTCAAGAAC	120
CATTTGGAAG GATCAAAGTA AAGGAAGTTC GTTATTTGAA GGAATTTAGA AATTTAAATT	180
CTAAGGATGC AAGGGAATAT GACTTGGCTT TATTAATTCT AGAAGAGCCC ATTGGTGCAA	240
AATTAGGGAC TTTGGGTCTT CCTACTAGTC AAAAAAATTT GACAGGAATA ACTGTGACTA	300
TCACAGGCTA TCCATCATAT AATTTTAAAA TTCATCAAAT GTATACAGAT AAGAAACAAG	360
TTTTAAGTGA TGATGGCATG TTCTTGGATT ACCAAGTTGA TACTTTAGAG GGGCTAGTG	420
GATCTACAGT TTATGATGCT AGTCACCGTG TAGTAGGAGT GCATACTTTA GGAGATGGAG	480
CTAATCAAAT TAACAGTGCA GTTAAATTAA ATGAACGAAA TTTGCCATTT ATTTAATCGG	540
TTCTTAAAGG TTACTCTCTT GAAGGATGGA AGAAAATAAA TGGTAGTTGG TACCATTATA	600
GACAACATGA TAAACAAACG GGTGGCAGG AGATAAATGA TACCTGGTAT TATTTAGACA	660
GTTCCGGTAA GATGCTTACA GATTGGCAAA AAGTCCATGG AAAATGGTAT TATCTCAATT	720
CAAAATGGAGC AATGGTTACA GGTAGCCAAA CTATCGATGG TAAAGTTTAT AACTTCGCTT	780
CATCTGGTGA GTGGATTAA TGTGGAGGA TATATAAAT GAAGCTTTTG AAAAAATGA	840
TGCAAAATCGC ACTAGCCACA TTTTCTTCG GTTTGTTAGC GACAAATACA GTATTTGCAG	900
ATGATTCTGA AGGATGGCAG TTTGTCCAAG AAAATGGTAG AACCTACTAC AAAAAGGGGG	960
ATCTAAAAGA AACCTACTGG AGAGTGATAG ATGGGAAGTA CTATTATTTT GATCCTTTAT	1020
CCGGAGAGAT GGTGTGCGC TGGCAATATA TACCTGCTCC ACACAAGGGG GTTACGATTG	1080
GTCTTCTCC AAGAATAGAG ATTGCTCTTA GACCAGATTG GTTTTATTTT GGTCAAGATG	1140
GTGTATTACA AGAATTGTT GGCAAGCAAG TTTTGAAGC AAAAAGTCT ACCAATACCA	1200
ACAAACATCA TGGGAAGAA TATGATAGCC AAGCAGAGAA ACGAGTCTAT TATTTGAAG	1260
ATCAGCGTAG TTATCATACT TTAATAACTG GTTGGATTTA TGAAGAGGGT CATTTGGTATT	1320
ATTTACAGAA GGATGGTGGC TTTGATTCGC GCATCAACAG ATTGACGGTT GGAGAGCTAG	1380
CACGTGGTTG GGTAAAGGAT TACCCTCTTA CGTATGATGA AGAGAAGCTA AAAGCAGCTC	1440
CATGGTACTA TCTAAATCCA GCAACTGGCA TTATGCAAAC AGGTGGCAA TATCTAGGTA	1500
ATAGATGGTA CTACCTCCAT TCGTCAGGAG CTATGGCAAC TGGCTGGTAT AAGGAAGGCT	1560
CAACTGGTA CTATCTAGAT GCTGAAAATG GTGATATGAG AACTGGCTGG CAAAACCTTG	1620
GGAACAAATG GTACTATCTC CGTTCATCAG CAGCTATGGC AACTGGTTGG TATCAGGAAA	1680
GTTCGACTTG GTACTATCTA AATGCAAGTA ATGGAGATAT GAAAACAGGC TGGTTCCAAG	1740
TCAATGGTAA CTGGTACTAT GCCTATGATT CAGGTGCTTT AGCTGTTAAT ACCACAGTAG	1800

1282

GTGGTTACTA CTTAACTAT AATGGTGAAT GGGTTAAGTA ATGAAGGCTA ATTGTAAACT	1860
GTGATGGATA CTTAACTTTG TATAATAGGT GGATAAAAGT CTTACAAATC AAAAAACGCA	1920
TAGTATCAAG GTTTTTCTGT ACTGCCCTCA AACAGTFAA CAATTAATTT ATCCGAAGgA	1980
TTTAGTTCTG TATTGCACAG GGCTAAGTCC TTTTAGTTTT ACCTTAATTC GTTTATTGTT	2040
GTAGTAATCA ATATAGTCTA TAATGGCTTG TTCCAATTGC TTAAGCGACT GAAACGACTT	2100
CTCATAACCG TAAACATTT CCGATTTTCA AATCCCAAAG AAGGACTCCA TCATACTATT	2160
GTCTGGGCTG TTTCCCTTAC GTGACATGGA TGCTTGAATT CCCTTACTCT CTAGGAACCG	2220
ATGATAAGAA TCGTGTGGT ATTGCCAGCC TTGGTCACTA TGGAGAATCG TATTCTCGTA	2280
GTGCTTCTCT GTGAATGCCT GTTCCAACAT TGTTTGTACT TGTCTAAGT TGGGTGAAGT	2340
TGAAAGATTA TAGCGGATAA TTTGCTATT AAAGCCATCT AAACTGGTG ATAAGTAAAG	2400
CTTTTGAGTA CTTGCTGGAA TGGCAAATTC TGTCACATCT GTGTAGCACT TTTCCATTGT	2460
TTTAGAGCCT TCAAATTGGC CTTGAATGAG ATTGC	2495

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 870 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TACCACCGTA TTCATCCAGC AAGATTGCCA TTTGTCTTTG GGTATTTTCGC AGTTCTTTTA	60
GCAAGTCATC CACAAAAATA GTTTCAGGTA CAAAAGTGG ATCTTGTAAG ATTCTCTTCC	120
AAACAATATT GTCAAAACCG TCCACAAAGC CTGCCTTAAG GAGACTCTTG GTGTGAATGA	180
TTCCAATTAC ATTGTCCTTA TCCCATCAT AAACCGGAT ACGAGAATAA TTTTGTTTTA	240
AAATACTTTG GATAATGGCT TGAATATCAT CCTGAATATC CACCATAAAG GCATCCGTTT	300
GAGGAACCAT AACCTCTCGT GCCATCAGTT CATCGAGCGA AAAGACACCT TGTAGCATCT	360
CAATCTCATC AGCATCCAAT GTTCTTTCAC TATTTGTCAG CATATAGGCA ATTTTCATCAC	420
GGGTCATCTT TTCATCCGCA TCATCGAATG ACATAGGAGT CAAATGGCTC AAGAAATTGG	480
TCGAAGCAGC TAAAAGCCAA ACAAAGGAC TGAATAGTT TCCGATCCCA ATGATAATCG	540
GCGCTGTACG AATTGCCAAG GCATCCTTTA GATTAAGAGC GATTCTCTTA GGATATAATT	600
CCCCAAAAAC GATGGAAATA TAGGTCAAAA ATGCCAAGGA TAGAAAAGTT GCCACGGCTT	660
GTGCTGTTTC GCCATTCCCA AGCCAAGAGC CAATCACACG TCCTAGAGTA TCAGTTAAAC	720

1283

TCGCCCCCTGA TAAGATTGTA ATCAGGGTGA TTCCTACCTG GATGGTTGAT AAAAAAGTGGT	780
TAGGATTTTC TAGTACCTTC AGCAGGCGGA TGTAGCGTCT GTCTCCTTCT TCCGCCTTTT	840
GTTCAACTCG GGCACGATTA AGAGAAACGG	870

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1245 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

CGTTCCCAAG AGCCCGCATT CTCATCGCCA ATGTCGTGAT TGATTTGGCC CTTTCTCCAA	60
AATCCAATC AGCCTATGTA GCTATGGATA AGGCATTGC TGACCTCAAA ACATCAGGGC	120
ACTTGCCCTAT TCCGCGACAC CTGCGTGATG GGCACACAG TGAAGCAAG GAACTGGGGA	180
ATGCCCAAGA CTATCTCTAT CCACACAAT ATCCTGGAAA TTGGGTCAAG CAAGACTATC	240
TGCCAGAAAA AATTCGTAAT CATCACTATT TCCAAGCAGA AGATACTGGT AAATATGAAC	300
GGGCTTTTGGC TCAAAGAAAG GAAGCTATCG ACCGTTTGCG AAAAATCTGA AATCCTTTTC	360
AAAAAATTGC ACTTTCCTCT TGATTTTTC TGAAGAAAGT GTATCATATA AATATAGAAA	420
CGCTGTGGTG TACGACTTCA CACTTAAGTC TTGACCGACT ATTTTGTGTA TTATTAGGGA	480
AACAAAAGTC TTCTAACAGC ATGTAGGCCG TCTCACACGG AAACAGCTTC AGTTAGAGCG	540
AGTTGCCAC CTGCTTAATT GCGCGGGTTC AATACAAACC GTGAAGTTTC GGCACCAATA	600
CAGCTTTTTT CTTCGCTCC TTAGCTCAGC TGGCAGAGCA GCGGACTCTT AATCCGTGGG	660
TCACAGGTTT GATCCCTGTA GGGGGCATAT AAATACAACA GGAAAAGCCT TATAATATAG	720
GGCTTTTTTT GCTTTCCTTT TAAAAATTGT CGTGCAATTT GCCGTGTTT TACAACAAAC	780
TTTTACAGC CATAAATCC TACTAATTT TTTCTCCAA GGTATGCCCC TAAACGTCAA	840
TCAACATGGA GATATCTTTA TGTCTAAAA TTTGGCTCTT TGTCAACTGT AGTGGGTGGA	900
AGTCAGCTAA GCTCGAGAAA GGACAAATTT TGTCTTTCT TTTTGATAT TCAGAGCGAT	960
AAAAATCCGT TTTTGAAGT TTTCAAAGT CCGAAAACCA AAGGCATTGC GCTTGATAAG	1020
TTTGATGAGA TTATTGGTCG CTTCCAATTT GCGGTAGAA TAGTGTAGTT GAAGGGCGTT	1080
GACGATTTTC TCTTGTTCCT TTGAAAGGT TTTAAAGACA GTCTGAAAA GAGGAGGAAC	1140
CTGCTTTAGA TTGTCCTCAA TGAGTCCGAA AAATTCTCTC GGTGCCTTAT TCTGAAAGTG	1200

1284

AAACAGCAAG AGTTGATAGA GCTGATAGTG ATGTTTCAAG TCTTG 1245

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1684 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

ATGCCTATGT AACTCCACAT ATGACCCATA GCCACTGGAT TAAAAAGAT AGTTTGCTG	60
AAGCTGAGAG AGCGGCACC AGGCTTATGC TAAAGAGAAA GGTGTGACCC CTCCTTCGAC	120
AGACCATCAG GATTCAAGAA ATACTGAGGC AAAAGGAGCA GAAGCTATCT ACAACCGCGT	180
GAAAGCAGCT AAGAAGGTGC CACTTGATCG TATGCCTTAC AATCTTCAAT ATACTGTAGA	240
AGTCAAAAAC GGTAGTTTAA TCATACCTCA TTATGACCAT TACCATAACA TCAAATTTGA	300
GTGGTTTGAC GAAGGCCTTT ATGAGGCACC TAAGGGGTAT ACTCTTGAGG ATCTTTTGGC	360
GACTGTCAAG TACTATGTCG AACATCCAAA CGAACGTCCG CATTGAGATA ATGGTTTTGG	420
TAACGCTAGC GACCATGTTC AAAGAAACAA AAATGGTCAA GCTGATACCA ATCAAACGGA	480
AAAACCAAGC GAGGAGAAAC CTCAGACAGA AAAACCTGAG GAAGAAACCC CTCGAGAAGA	540
GAAACCGCAA AGCGAGAAAC CAGAGTCTCC AAAACCAACA GAGGAACCAG AAGAATCACC	600
AGAGGAATCA GAAGAACCTC AGGTCGAGAC TGAAAAGGTT GAAGAAAAAC TGAGAGAGGC	660
TGAAGATTTA CTTGGAAAAA TCCAGGATCC AATTATCAAG TCCAATGCCA AAGAGACTCT	720
CACAGGATTA AAAAATAATT TACTATTTGG CACCCAGGAC AACAATACTA TTATGGCAGA	780
AGCTGAAAAA CTATTGGCTT TATTAAAGGA GAGTAAGTAA AGGTAGCAGC ATTTTCTAAC	840
TCCTAAAAAC AGGATAGGAG AACGGGAAAA CGAAAAATGA GAGCAGAATG TGAGTTCTAG	900
TTCTCATTTT TTTTCATGAAA ATGTGCAAAA TATAGTAGAT TGAACTAGA ATAGTATACC	960
TCTACTTCTA AAACATTGTT AGAAATCGAT TTGACTGTCC TGTTCCTATT TCATTTTACT	1020
ATATCTTAAC AGATAGTGTA AATAAGATA AACTATTTAC TGGCTAATTA ATCAGTTAAA	1080
CACTAGTTAA GGAGTAATGA TGAAAAAAG AACAATACTA TTATTGATGG CCAGTCTGTT	1140
AGCTCTTGTC TTAGGAGCAT GTGGTTTCTT GGACATATTG ATCCTGGATC ATTCTCATCA	1200
GGATTACTCT TTAAGTCTAT TTTAGAAACT GGGGTGGTTT GATGGAAAGT ATTGGTCTTG	1260
TTATCGTTTC ACATTCCAAA CACATTGCAG AAGGTGTTGT TGAAGTATT AGTAAAGTAG	1320
CTAAAGATGT TCCGATTACT TATGTAAGAG GAACCGAGGG CGGAGGAATT GGAACGAGTT	1380

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TTGAACAAGT AGATAGGGTT GTTCCGAAA ATCCAGCAGA TACTTTACTT GCCTTTTTTG	1440
ACCTAGGTTC TGCTAAATG AACTTAAAA TGGTGAAGTGA TTTCAGTGAT AAAAGTATCA	1500
TCATCAACAG GGTTCCAATT GTAGAAGGTG CCTATAATGC AGCTGCTCTT CTTCAGGCTG	1560
GTGCAGAACT GTCAGTTATT CAAACACAGT TaGCGGAgCt TGAAATCAAT AAATAAGGAA	1620
TTTTACTATA ACTCTTTTTA TAGATAAGCT ATTGaTTATC TCAACTATAA TAATGTTAAG	1680
TnAA	1684

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 970 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AGGAGTGGAG AnATATGAAG ACACAAATTT TCACATTATT GAAAATCGTT GCTGAGATTA	60
TTATTATTTT GCCATTTCCTA ACTAATCTAT AAGTCTTTTA TATTGCTGAA AACGCAATTC	120
AAAAAGGGCT ATTAATTCTG GATTTTCTAA TACCTGCAGA GATTGGATAA AGCGTCAAT	180
CTCTTTTGA TTGCTTCCCT TTGTTTGAAG AAAGACACTC ATCTTCTTTA AAAATTGCCA	240
CGATACTTTT TCAAAAACAT CATACGGTCG TAACATCCTC TCCAACCTCGG CTTCGAAGAT	300
TGGGATGTAG GAGAAAAGTT TTCGCTCCAT GAGTCTGAT AAGATATTTA AGAGTCCTTG	360
CTTCATATAC AATCGATTGT GTACTAACTC TTTAAATCTT TTGGATTTT CGAGTAAGGA	420
GGTTGATAAA AAAATCAGAT CTTGATTGCT CAAGAAGGCC ATGGTATTGC AAAAGAGATA	480
GAGTTCAAAC CAGGTCCAAG ACTCGATAGC ATAGAGATAG GTGGTCAAAA ACTCGCTATC	540
CTCCTCTGCT AGTGGGTAGC TTTTATTTAG TGAATGGATG GCATCTTTAA TCACGATGGC	600
ATTCAAACGA CGATAGGTCT GCGCCATCTG TTCTTGATCG ACTTCCTCCA ATAGCTGCTC	660
TAAAGCAGCT ATATCCTGAT GGGCAAAGCG ATTCAACAAC TTTCGACCGA TTCGCATATG	720
TGGAGATTCT TGATAGTTGT TGAGCTTGTG CCCAACTCA TCAAAGGTCA CATTTATACC	780
TTGGATAGCT AGAATCAACT TATCCGCAGA CAGCATAGAC TGCCCTAGTT CAAACTTGGA	840
CAACTGAGAA GCTGTTAGAC CCTCACAAGC CACATCTGAC TGCTTGAGCT TTCTCGCCAA	900
ACGTAATTCC TTGTAAATTT CCCCCAGTTC CATCTCTCA ATCATCTGAC CACCTCCTAG	960
CTTTTGCAAG	970



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(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2996 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

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GTTGACCACG GGTAAACTA CCCTAACTGC AGCTATCACA ACTGTTTGG CACGTCGCTT      60
GCCTTCATCA GTTAACCAAC CTAAAGACTA TGCCTCTATC GATGCTGCTC CAGAAGAACG      120
CGAAGCGGGT ATCACTATCA ACACTGCGCA CGTTGAGTAC GAAACTGAAA AACGTCACCTA      180
CGCTCACATC GACGCTCCAG GACACGCGGA CTACGTTAAA AACATGATCA CTGGTGCTGC      240
TCAAATGGAG GGAGCTATCC TTGTAGTAGC TTCAACTGAC GGACCAATGC CACAAACTCG      300
TGAGCACATC CTTCTTTCAC GTCAGGTTGG TGTAAACAC CTTATCGTCT TCATGAACAA      360
AGTTGACTTG GTTGACGACG AAGAATTGCT TGAATTGGTT GAAATGGAAA TCCGTGACCT      420
ATTGTCAGAA TACGACTTCC CAGGTGACGA TCTTCCAGTT ATCCAAGGTT CAGCACTTAA      480
AGCTCTTGAA GGTGACTCTA AATACGAAGA CATCGTTATG GAATTGATGA ACACAGTTGA      540
TGAGTATATC CCAGAACCAAG AACGTGACAC TGACAAACCA TTGCTTCTTC CAGTCGAGGA      600
CGTATTCCTA ATCACTGGAC GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTATCGT      660
TAAAGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA GAAACTCAA AAGCAGTTGT      720
TACTGGTGTT GAAATGTTCC GTAAACAACT TGACGAAGGT CTTGCTGGAG ATAACGTAGG      780
TGTCCTTCTT CGTGGTGTTT AACGTGATGA AATCGAACGT GGACAAGTTA TCGCTAAACC      840
AGGTTCATC AACCACACA CTAAATTCAA AGGTGAAGTC TACATCCTTA CTAAAGAAGA      900
AGGTGGACGT CACACTCCAT TCTTCAACAA CTACCGTCCA CAATTCTACT TCCGTACTAC      960
TGACGTTACA GGTTCATCG AACTTCCAGC AGGTACTGAA ATGGTAATGC CTGGTGATAA     1020
CGTGACAATC GACGTTGAGT TGATTCAACC AATCGCCGTA GAACAAGGTA CTACATTCTC     1080
TATCCGTGAG GGTGGACGTA CTGTTGCTTC AGGTATGGTT ACAGAAATCG AAGCTTAATT     1140
CGATTTAGTT CCCAGAAGAA CAATTATTTA AGTTAGACAC TAAAAGAATC TTGCTTGGCA     1200
AGGTCTCTTT TTTAGATATT GAACTAATAC TCAATGAAAA TCAAAGAGCA AACTATAATA     1260
TATTGAAACT AGAATAGTAC ACATCTACTT CTAAAACATT GTTAGAAATC GATTTGACTG     1320
TCCTGATCGA TTTGTCTTGT TCTTATTTCA TTTTACTATA GAAAGTTAGC TACAGACTGC     1380
TCAAAACATT GTTTTtaggt TGTAGATAGA ACTGACGAAG TCAGtAACAT CTATACGACA     1440

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AGGCGAAGCT GACGCGGTTT GAAGAGATTT TCGAAGAGTA TAATACTAGA CTAAAATCAA	1500
AAAGCATTAT ACAATAGTAA TATGAAATCA ATTAAGAAG AAATCCAAAC CATCAAAACA	1560
CTTTTAAAAG ACTCTCGTAC AGCTAAATAT CATAAACGCC TTCAAATCGT TCTATTTTCGT	1620
CTGATGGGCA AATCTTATAA AGAGATTATA GAACTTTTAT AGTGGTTTGA AATAAGATGT	1680
GAACAACTCT ATCAGGAAAG TCAAACAAAT TTATAGAAAT ATTTTAGCAG CCAAGGTGTA	1740
CTGTTATAGA TTCAATACAC TTTAGACTGT AATCAACAA CGATTTGGCG AAATGTAAAA	1800
AATATGAGGA GTTCGGACTC GACTCTCTCC TTCAGAAAC ACGTGGTGGT CGTAACCATG	1860
CTTATATGAC GGTGAGCAA GAGAAAGTCT TTCTTGCCCG CCATTGAAG GCTACAGAGG	1920
CAGGAGAATT TGTTACAATT GATGCCTTAT TTCAGGCTTA TAAAAAGGAG TTAGGTCGTT	1980
CCTACACACG TGATGCCTTC TATCAACTGT TGAAGCGCCA TGGTTGGCGA AATATTACGC	2040
CACGTCCAGA ACATCCTAAG AAAGCAGATG CTCAAACCAT TGTCGCGTCT AAAAATAAAG	2100
TCTCAATTCA AGAAGACAAG TGAAGTCAC CCCAAAGTT AGACAGAAA AATCTAACTT	2160
TTGGGGTGTT TTTATTATGA AATTAAGTTA TGATGATAAA GTTCAGATCT ATGAAGTTAG	2220
AAAACAAGGA TATAGCTTAG AGAAGCTTTC AAATAAATTT GGGATAAACA ATTCTAATCT	2280
TAGGTACATG ATTAAATTGA TTGATCGTTA CGGAATAGAG TTCGTCAAAA AAGGAAAAA	2340
TCGTACTACT TCTCCTGATT TAAAACAAGA AATGATTCAT AAAGTCTGAC ATGAAGGCTG	2400
GACTAAAGAT AGAGTTTCTC TTGAATACTG TCTCCCAAGT CGTACCATAC TTCTTAACTG	2460
GCTAGCACAA TACAGGAAAA ACGGGTATAC TATTGTTGAG AAAACAAGAG GGAGAGTACC	2520
TGAGAGCGGA GAATGCCATC CTAAAAAGT TAAGAGAACT CCGATTGAAG GAGGAAAAAG	2580
AGAAAGAAGA AAGACAGAAA TTATTCAAGA ATTAATGACT GAGTTTTCGT TAGATATTCT	2640
TCTAAAAGCC ATTAAACTAG CTCGTTTGAC CTACTACTAT CACTTGAAAC AGCTAGATAA	2700
ACCAGATAAG GACCAAGAGC TTAAAGCTGA AATCAATCC ATTTTATATCC AACACAAGGG	2760
AAATTATGCT TATCGTCGGA TTTATTTAGA ACTAAGAAAT CGTGGTTATC TGGTAAATCA	2820
TAAAAGAGTT CAAGGCTTGA TAAAAGTACT CAATTTACAA GCTAAAATGC GACAGAAACG	2880
AAAATATTCT TCTCATAAAG GAGACGTTGG CAAGAAGGCA GAGAATCTCA TTCAAGGACA	2940
ATTTGAAGGC TCTAAAACAA TGGAAAAGTG CTACACAGAT GTGACAGAAT TTGCCG	2996

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 837 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

1288

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTTATCAACT CCCGACATGG CTCTCAGACC AATCCAAATC CCTAAAAAA TCAGAACAAG	50
GATGGTGGTC AAGATCAAAC TCTCGAAATA TAAAGAAAAT AGTTGCAGTA GCATGATTTC	120
TCTCATTCT ATCTTTTTTA AAGAGTAAAC TCAGCTAGTC CAACTAACTG AGTTTTCCTT	180
TATCTATTAT ATCAAATATA AGTCCGTTTG TAACTAGCGA AGAATTCTTT TGTCCGCTCT	240
TCTTTAGGGG TGTGGATAAT CTCATCCGGA GTTCCAGACT CGATGATTTT CCCCTTATCT	300
AAGAAGAGAA TTTTATCCGC AACTTGGGCT ACAAAGGACA TGTCATGACT GACCAAAATC	360
ATGGTCTGAC CTGACTTAGC AGCATCTGCA ATAGACTTTT CTACTTCACC GACCAATTCT	420
GGGTCAAGGG CTGAAGTTGG TTCGTCTAAG AGCAAAACAT CTGGTTTCAT AGCAAGCGCA	480
CGCGCTAGGG CAACCCGTTG CTTCTGTCCA CCTGATAAAT GCGGAGGATA ATGGTTTTCA	540
CGGTCCGAAA GCCCAACCTT AGCCAACTCT TCCTTGGCAA TCTTAGTCGC TTCTTGGTCA	600
GATAATTCTT TGACAACAAC CAAGCCTTCT TTCACATTAT CAAGTGCTGT TCGGCGTTCA	660
AACAAATTAA ACTGTGGAA AACCATAGAC AACTTACGAC GTAGGGCAAG GATTCTTCTT	720
TGAGTGATTT TAGAAAAATC AACTGAAAAA CCATCAATCT GAATAGAGCC ACTGTCAGGT	780
GTTTCTAGAT AATTGAGACT GCGAGAAAGG TTGATTTTCA GCTCTGAAGA CCAATCA	837

## (2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 868 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CCGAACAAAA TGGGCTAATT AGATTATAGT AAGAAAGGTA AGTTAAAAAT GAGAAATTGCA	60
ATTGGATGTG ACCACATCGT AACTGATGAA AAAATGGCGG TTTCAGAATT TTTGAAATCA	120
AAAGGATATG AAGTCATTGA CTTTGGTACC TATGACCATA CACGGACTCA CTACCCAATC	180
TTTGGTAAAA AAGTAGGGGA AGCTGTAAC TACGGTCAAG CTGATCTTGG AGTATGTATC	240
TGTGGTACTG GTGTTGGTAT CAACAACGCT GTAAATAAAG TTCCAGGTGT TCGTTCTGCC	300
TTGGTTCGTG ATATGACAAC AGCCCTTTAT GCTAAAGAAC AATTGAACGC TAACGTTATT	360
GCTTTTGGTG GTAAATTAC TGGTGAATTG CTTATGTCTG ATATCATCGA AGCTTTCATC	420

1289

CATGCTGAAT ACAAACCAAC TGAAGAAAAC AAAAAATTGA TTGCGAAAAT TGAACATGTT	480
GAAAGTCACA ATGCTCAACA AACAGACGCA AACTTCTTTA CAGAATTCCT TGAGAAATGG	540
GATCGTGGAG AATACCACGA CTAAGAGGTG ACCTATGATT TTAACAGTCA CAATGAACCC	600
ATCCATCGAT ATTTCTATC CCTTGGATGA GTTGAAGATT GATACTGTCA ATCGTGTGGT	660
GGATGTAACC AAAACGGCTG GTGGTAAGGG ACTCAATGTT ACCCGAGTAC TTTCAGAATT	720
TGGCGATTCT GTTCTTGCTA CTGGTTTAGT GGGTGGCAAA CTTGGTGAGT TTTTGGTTGA	780
ACATATCGAT AATCAAGTAA AGAAAGATTT CTTCTCAATT AAGGGAGAAA CTCGTAACGT	840
TATCGCTATT CTCCACGGAG ACAACCAA	868

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3744 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CCGTTCAAAG TCTTCATAAG ACTCGAAAGT CACAGTCTTT TCGTTCTTGC TGGCATCTAT	60
ATAGGTAATT TCAATCATGT TTAAACTCC TTTGTTTAAT GCTAACTTTA TTTTACTCCT	120
TATAAAGAG AATGTCAAGA AAAATGATTG CGCACGCAAC TTTTTTTAAA ATCATCTTAA	180
ATCAAGAAAT CCAAACCTGC TTCCAAGCTT TCTTCGACAG TCTTTTGTAG CGAGGCCAGT	240
GTCTTTTGCC CATCATTTGT CAGGCAGATA AACTAGAGC GTCTATCTTG ATGGCAACAC	300
ATGCGACTGA GTAGACCGCA ATTTTGTAGCT TCCAAGCGAG CCACCATCCT AGAAACTGCG	360
CTCGGGCTCA GATGAAGCTT ATCTGGCAGG TCAATCTGGC GTAGAGATTT TTCTTCAGCC	420
AAGTCCAGAT AGTAGAGCAG GTAGAACTCT TTCAAGGTCA GACTTTGCTC GCTCTGTTGG	480
GCAATGGTCT CTTCCAAGAG ACTTTCAATT TCTTCTGAC GCCGATTGAA GTCAAACCAT	540
TTTTCCAAAT AGGTCATAGT GTCTCCTTTC TTTTGTAGAGT CATAAATAGA AGAAAGTCCA	600
TTAACGGGCA GTCTCTGCGT CACAAGATGA TTGCGCATGC AATAATTATA CTACTTTTCA	660
AGAAATGCTGG CAAGCTCTGT TTTTGTAGTG TTTTATTTTT GTGTGAATAA TGGGGGAATC	720
CTATTGTTTC AATTCTAAC TCCTTATCAC ATTCAATTC AGATTTTATT TCATTCTCT	780
ATCTATAGTT GCTTAGTTTA AAATAAGCAT GGTCTAATAA AGCTATGCAT ATAGTACTGA	840
TTTAAACAA GGAGCATTAG ATTCCATTAA AGGAGGGCAC AGACATGTCG AGGCGGCCAA	900

1290

AGTTTTTCAT GTCGGCGTCA GAACTCTCTT CACGTGGGAA AAGAAAGACG TAAACAAGGG	960
AACTTAGAGC GGAAAAAGCG AGTCGTCAAA AAGCGTAAGA TCCCTTTAGA AGAATTGAAA	1020
GCCTTTGTAG AGGCTCATCC AGACGCTTTT TTACGGGAAA TTGCGGCCCG TTTTGATTGT	1080
GCTTTGCCCT CCGTATGGGC AGTTTAAAG CAGATTAAGG TCATTTTAAA AAAGACGACC	1140
AGTTTTAGGG AACAAAAGCC TGAGAAAGTT TCTGAGTTTC TTGATATTTT GGATAACCTA	1200
AAAGATTTAC CAGTCCTATA TATGACGAA ACGGGAATCG ACCGCTACCT CTATCGTCCT	1260
TATGCAGGGG CTCCTAGAGG GGAGAAAGTC TATGGCAAGA TTAGCGGACG GCGTTTTGAG	1320
CGGACTAATG AGGTGGAGCA AAAACTCAAT GGTAGTTTTC TAATCAGATA TATTGATTCA	1380
CAAATTAGAG AATGAAAGAA TAATTATGCA TAAAAATAGG AATATAAACC AAAAATTAGC	1440
TGATTTATAC TCATTTGCGT GTCTTTATAA AAAACTTATC TTATAATATA TATATATATA	1500
TATACAAAAT AGTAAATGC TTTTTTTTTT TAGCAAAAAT ACCTCAAGTT TCTTGCTATT	1560
TTGGGTTCCT TATTCATATA TTATAGTATG GTAATTTATT TATATCCATA CATGAAAATA	1620
ATACTCGAAA GGAAATTTCA AAATATTTTT TAGACCTCAG AAGGGTGAAT ATAGAGAAAC	1680
AGACCGAGTA ACTCGGTTCA AATTAATCAA ATCAGGGAAG CATTGGCTAC GGGCCTCGAC	1740
TTCTCTTTTT GCGTTGTTTA AGGTCTTGCG AGGTGGTGT GATACTACTC AGGTCATGAC	1800
CGAAACGGTA GAAGATAAAG TAAGTCATTC AATTACTGGG CTTGATATCC TCAAGGGGAT	1860
AGTTGCTGCG GGAGCTGTCA TAAGTGGAAC CGTTGCAACT CAAACGAAGG TATTTACAAA	1920
TGAGTCAGCA GTACTTGAAA AAAGTGTAGA GAAAACGGAT CTTTGGCAA CAAATGATAC	1980
AGTAGTTCTA GGTACGATAT CTACAAGTAA TTCAGCGAGT TCAACTAGTT TGTCAGCTTC	2040
AGAGTCGGCA AGTACATCTG CATCTGAGTC AGCCTCAACC AGCGCTTCGA CCTCAGCAAG	2100
TACAAGTGCA TCAGAATCAG CAAGTACATC GGCTTCGACA AGTATTTCTG CATCATCTAC	2160
TGTGGTAGGT TCACAAACAG CTGCCGCTAC AGAAGCAACT GCTAAGAAGG TCGAAGAAGA	2220
TCGTAAGAAA CCAGCTAGTG ATTATGTAGC ATCAGTTACA AATGTCAATC TCCAATCTTA	2280
TGCTAAGCGA CGCAAGCGTT CAGTGGATTC CATCGAGCAA TTGCTGGCTT CTATAAAAAA	2340
TGCTGCTGTT TTTTCTGGCA ATACGATTGT AAATGGCGCC CCTGCAATTA ATGCAAGTCT	2400
AAACATTGCT AAAAGTGAGA CAAAAGTTTA TACAGGTGAA GGTGTAGATT CGGTATATCG	2460
TGTTCCAATT TACTATAAAT TGAAAGTGAC AAATGATGGT TCAAAATTGA CCTTTACCTA	2520
TACGGTTACG TATGTGAATC CTAACAAAAA TGATCTTGGT AATATATCAA GTATGCGTCC	2580
TGGATATTCT ATCTATAATT CAGGTACTTC AACACAAACA ATGTTAACCC TTGGCAGTGA	2640
TCTTGGTAAA CCTTCAGGTG TAAAGAACTA CATTACTGAC AAAAATGGTA GACAGGTTCT	2700

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ATCCTATAAT ACATCTACAA TGACGACGCA GGGTAGTGGG TATACTTGGG GAAATGGTGC	2760
CCAAATGAAT GGT'TTCT'TTG C'TAAGAAAGG ATATGGATTA ACATCATCTT GGA CTGTACC	2820
AATTACTGGA ACGGATACAT CCTTTACATT TACCCCTTAC GCTGCTAGAA CAGATAGAAT	2880
TGGAATTAAC TACTTCAATG GTGGAGGAAA GGTAGTTGAA TCTAGCACGA CCAGTCAGTC	2940
ACTTTCACAG TCTAAGTCAC TCTCAGTAAG TGCTAGTCAA AGCGCCTCAG CTTCAGCATC	3000
AACAAGTGCG TCGGCTTCAG CATCAACCAG TGCCTCGGCT TCAGCGTCAA CCAGTGCGTC	3060
AGCTTCAGCA AGTACCAGTG CTTCAGTCTC AGCATCAACA AGTGCTTCAG CCTCAGCATC	3120
GACAAGTGCC TCGGCTTCAG CAAGCACATC AGCATCTGAA TCAGCGTCAA CCAGTGCTTC	3180
GGCTTCAGCA AGTACCAGTG CTTCAGCTTC AGCATCAACC AGCGCCTCGG CCTCAGCAAG	3240
CACCTCAGCT TCTGAATCGG CCTCAACCAG CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC	3300
TGAATCGGCC TCAACCAGCG CCTCAGCCTC AGCATCAACG AGTGCTTCGG CTTCAGCAAG	3360
CACAAGCGCC TCGGGTTCAG CATCAACGAG TACGTCAGCT TCAGCGTCAA CCAGTGCTTC	3420
AGCCTCAGCA TCAACAAGTG CGTCAGCTCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA	3480
ACGAGTGCGT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT CAGCAAGCAC CTCAGCTTC	3540
GAATCGGCCT CAACCAGTGC GTCACCTCAG CATCGACAAG CGCCTCAGCT TCAGCAAGTA	3600
CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG	3660
CATCAACCAG TGCGTCAGCC TCAGCAAGTA CTAGTGCATC GGCTTCAGCA TCAACCAGTG	3720
CCTCGGCTTC AGCGTCAAAC AGTG	3744

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 795 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

CGATAAAGAG GCCTTGAGTA ATCTCAATTT GCAGATTGAA AATGGAGAGA TTATGGGCTT	60
GATTGGTCAT AATGGGGCTG GAAAATCGAC CACTATAAAA TCCCTAGTCA GTATCATTTT	120
ACCCAGCAGT GGTCGTATTT TGGTAGACGG TCAGGAGTTA TCGGAAAATC GCTTGGCTAT	180
TAAACGAAAG ATTGGCTACG TAGCAGACTC GCCTGACTTA TTTTACGCT TAACGGCCAA	240
TGAATTTTGG GAATTGATCG CCTCATCCTA TGATCTGAGT AGATCTGACT TGGAGGCTAG	300

1292

TCTAGCTAGG CTATTGAACG TTTTGTGATTT TGCTGAAAAT CGCTATCAGG TTATTGAAAC	360
TCTTTCTCAC GGAATGCGTC AGAAAGTCTT TGTCATCGGA GCACTCTTGT CTGATCCCGA	420
TATTTGGGTC TTGGATGAAC CCTTGACTGG TTTGGATCCC CAGGCTGCCT TTGATTGAA	480
ACAGATGATG AAGGAACATG CACAAAAAGG GAAGACAGTC TTGTTTCAA CTCATGTCTT	540
AGAGGTGGCA GAGCAAGTCT GTGATCGGAT TGCCATTTTG AAAAAGGGC ATTTGATTTA	600
TTGTGCTAGT GTAGAGGACT TGAGAAAAGA TTACCCAGAC CAGTCTTTGG AAAGTATCTA	660
CCTTAGTCTT GCTGGTAGAA AAGAGGAGGT TGCGGATGCG TCTCAAGGTC ATTAAAAAAT	720
TAGTTGATAT CAATATCCTT TATTCATCTC AAGAAGCTAA TCTGGCTAAT CTACGAAAGA	780
AGCAGGCTAA GAATC	795

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2231 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TGTTAATGTG CTTGGCAGCw TCCTTGACAC TGCTACTACC ATTTCCCATA GCGACCGACA	60
TACCAACGCC AGCCAGCATT TCAAGATCAT TATCTGAGTC ACCAAAAGCC ATGACTTGGT	120
TGAGGTCAAA GCCATATTCT TTCCCAACTC GGCGAATGCC TTCTAATTTA GAATTTCCCT	180
GATTGATGAC ATCCGATGCA AAAGGATTGC TACGTGTCAA TTTCAAGTCT TCAAAATCAG	240
CTGCCGCCTT CTCAGATTCT TCTGGTGTC ATCAGCATCAA AACTTGGTAG ATAGGCTGAT	300
TCATCAGGTG AAGCAGGTCC TCTTCCTTTT GGGGAACAAC CTTGCTGACC ATGCGATTAA	360
AAGACTGACT CACCGTCCGA GTTAAACAG AGGGAACGAA GCGACTAATT CGTTGGGAAA	420
AAGAACCCAG ACCAAAGGAC ATGATTTTAG AACCAACAT GGCATCCTTG GTCCCTAGAG	480
CAATCTCCGT GCCCTCTTTT TTAGCATAGC TAATTAGATG GCGCAAATGT AACTTGAAA	540
TAGGGCTCGT GAACAAGACT CTGTCTTTAC TAAAGATATA CTGGCCATTA TAGGTTACCG	600
CAAAATCCAG ATCCAAATCG TCCATCAATT CCTTAACAAA AAAAGGTCCT CGCCCTGTCG	660
CTACGCCAAC TAGTACCCCT TGTTCTTTGA CAATCTTAAT CGCATCCTTA GTGGATTTC	720
AAACACTCTT GCGATTGTTG ACCAAGGTT CATCGATATC AAAAAAACA GCTTTGACTT	780
CCATCCTATC CCAATCTCCC CTTTGTGAT ACAATGATTA TACCACATTT CAGAAAGAGT	840
GAGTAAATCA TGCCTAAGAA AATCCTTGTT TTACATACGG GTGGAACATAT TTCCATGCAG	900

1293

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GCCGATGCTT CTGGCGCTGT TGTGACGAGT TCAGATAATC CCATGAACCA TGTGTCCAAC      960
CCACTTGAAG GAATCCAAGT CCACGCCTTG GACTTTTTTA ACCTTCCAAG TCCCCATATC      1020
AAACCCAAAC ATATGCTGGT CCTCTACCAG AAAATTAAAG AGGAAGCAGA TAACTACGAT      1080
GGAGTGGTGA TCACACACGG AACCGATACT TTAGAGGAAA CAGCCTATTT CCTTGATACC      1140
ATGGAAGTTC CCCATATGCC TATCGTTCTA ACAGGAGCCA TGCCTACTCC AATGAGCTCG      1200
GTAGTGATGG TGTTTATAAT TACCTAAGTG CTTTACGAGT GGCCAGCGAT GACAGGGCTG      1260
CTGACAAAGG AGTTTGGTC GTTATGAACG ATGAAATCCA CGCTGCCAAG TATGTCACCA      1320
AAACACATAC GACTAATGTC AGCACCTTCC AGACTCCAAC ACATGGCCCC CTGGTCTCA      1380
TCATGAAACA GGAAATCCTC TACTTCAAAA CAGCTGAACC TCGTGTTCGC TTGACCTTG      1440
ATCACATACA AGGTTTAGTC CCTATCATCT CGGCTTATGC TGGTATGACA GATGAGCTGA      1500
TTGATATGCT GGATTAGAA CACTTGGACG GTTTGATTAT CCAAGCCTTC GGAGCTGGTA      1560
ATATTCCTCA AGAAACGGCT CAAAAATTAG AAAGCCTTCT GCAAAAAGGA ATTCAGTCG      1620
CTCTGGTATC ACGATGCTTT AACGGTATTG CCGAGCCTGT TTATGCATAC CAGGGTGGGG      1680
GCGTACAGTT GCAAAAAGCA GCGTTTTCTT TTGTTAAAGA ACTCAACGCC CAAAAGCTC      1740
GCTTGAACCT CCTCATCGCC CTCAATGCCG GACTAACAGG ACAGGCTTTG AAAGACTATA      1800
TGGAAGGCTA ATACTCTTCG AAAATCTCTG CAAACCACGT CACGTCGCCT TACCGTATGT      1860
ATGGtACTGA CTTGTCAGT TTCATCTACA ACCTCAAAAA CATGTTTGA GCTGACTTCG      1920
TCAGTTCTAT CTACAACCTC AAAACATGT TTTGAGCTGA CTTGTCAGT TCTATCTACA      1980
ACCTCAAAAA CATGTTTGA GCTGACTTCG TCAGTTCTAT CTACAACCTC AAAACATGT      2040
TTTGAGCTGA CTTGTCAGT TCTATCTACA ACCTCAAAAA CATGTTTGA GCTGACTTCG      2100
TCAGTTCTAT CTACAACCTC AAAACATGT TTTGAGCTGA CTTGTCAGT TCTATCTACA      2160
ACCTCAAAAA CATGTTTGA GCTGACTTCG TTAGTTTCAT CTACAACCTC AAAACATGT      2220
TTTGAGCTGA C

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(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1310 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:



1294

GAGTCAAAGG CTCCGAGGTT GACTTTTTAC AAGGGGACAG GTGAATATTA TCTAGACCTG	60
TCAGAAATTC TCTTCTTTGA AACAGAAGGG AGCAAGATCT ACGCTCATAA CCAGAAGGAA	120
GCTTATGAGG TTCGCCTCAA GCTCTATGAG TTGGAGTCTA TCTTGCCTCG CTATTTTAAAT	180
CGAGTTTCCA AGTCAACGAT CGCAAACATC CGTCAGATTT ACTCAGTGGA CAAGTCCTTT	240
TCAGGAACGG GCACCATTTT CTTTATCAG ACGCACAAGG AGGTTTCATGT CTCACGGCAT	300
TACCAATCCC TCCTAAAAGA AAATCTAAGA AACATGAGGT AAAAAACATG AAAAAGAAAG	360
CATTTGGTAT TGTTTTATTG GTTTTAGCAG CTTGGATCTT GCTGCAAGGG AATTTTGGAA	420
TTCTTCTTTT GGATGGTAAA ATATGGCCTT TACTAGGTAT TGTTTTTTTT GCTTATAAGT	480
CCATTTGAGTC CATCTTAGA CGTCATCTCA CTTCCGCAGT TTTTACAGGT TTACTGGCGC	540
TCATCATTCG AAATTACGCT TATGACTTGT TACCAGTTAC CAATCATTCCT CTTATTTGGG	600
CTAGCATCTT GGTGGTACTT GGTGTTGGTT ATCTGACGCA TTCAAGTAAG TTCTGGAATG	660
AAAAAAATG GTGGTACAAT GGGAAAAAAA CAGTCGTCAC GGATAAGGAA GTCGCTTTTG	720
GTAGCGGGAC CTTCTATAAG CAAGATCAAG ATCTCGTAGA TGACCAAGTG GAAGTCGCTT	780
TTGGGGATGC TAAAACTAC TATGATAATG CAGAGATGCT AGGTGATTTT GCAACTTTAA	840
ATATTGAAGT GGCCTTCGGG AATGCAACCG TCTATGTTCC ACAACACTGG CGTGTAGATT	900
TGAAAGTAGA AACCTCCTTT GGTGCAGCTA AGGCTGACGC TCCTGTAGCC CCAACCAGCA	960
AAACCTTGAT TATCCGTGGA GATGTGGCTT TTGGGAAGTT GGAAATTGTC TACGTTAAAT	1020
AAAAAATCT TCACTTCAAC CATCAAATA GACGTACTAA GAGTAGGAAA TTGATGCCTT	1080
GCTCTGATTT CAGTTCTATG GTTGTTAGAC TTTAAAAAAT GAAATGCTGC CTTTAAAAGT	1140
TGTATATTTT TCGATATTTT GGCTTTTACG TTTGATGTAT CTATGTACTA CAGCGTAGAT	1200
GATGTAGTGT CAAATGCTTT TAAAAACGG ATGATATTGG ACAGTTTTTT TGCCTTTAAT	1260
TGCTCAGGAA CCATGAAAGT CAGTACCTGG GTTTATGACA AGGGAGAATG	1310

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5922 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

ACTCTGATTT GATTGGAACG ACAGTCGGTG CCATTGCAGT TACTTCAAAC GTAACGACTT	60
ATGTTGAGTC TGCTGCTGGT ATCGGTGCAG GTGGACGTAC TGGTTTGACA GCCTTGCTTG	120

1295

TAGCTATCTG TTTTGCGATT TCAAGCTTCT TTAGCCCACT TCTAGCGATC GTACCAACAG	180
CGGCTACAGC TCCAATCTTG ATTATCGTTG GGATTATGAT GCTTGGTAGC TTGAAAAATA	240
TCCATTGGGA TGATATGTCT GAAGCAGTTC CTGCCCTCTT CACATCTATC TTTATGGGAT	300
TCAGCTACTC TATCACTCAA GGGATTGCAG TTGGTTTCTT GACTTACACT TTGACTAAGC	360
TTGTTAAAGG TCAAGTTAAA GATGTTTCATG TCATGATTTG GATTTTGGAT GCCTTGTTTA	420
TCCTTAACTA CATCAGCATG GCCTTATAAT AGAATGACCC AGGGGGATTT CCCCCCTTTT	480
TTAATACAaG GAGATAGGTG ATGAAAGAGA AAAATATGTG GAAAGAATTG TTGAATCGTG	540
CAGGCTGGAT TTTGGTCTTT TTA CTGCTGCGG TCCTTTTATA TCAGGTTCCT CTAGTGGTTA	600
CCTCTATTTT GACTTTAAAA GAAGTAGCCC TGCTACAGTC AGGGCTGATA GTTGCTGGCC	660
TTTCAATTGT GGTCTCGGCT CTATTTATTA TGGGAGCTCG TAAACCAAG TTAGCTAGTT	720
TTAATTTTTC TTTTCTTAGA GCTAAAGATT TGGCACGTTT GGGCTTGAGT TATCTAGTTA	780
TTGTGCGGTC AAATATACTT GGTTCCTTTT TATTGCAACT GTCAAATGAG ACGACAACAG	840
CTAACCACTC TCAGATTAAT GATATGGTTC AAAATAGTTC GTTGATTTCCT AGTTCTTCTT	900
TGCTAGCCTT GCTTGCTCCG ATTTGTGAGG AAATCTTGTG TCGTGGGATT GTTCCTAAAA	960
AGATTTTCCG AGGCAAGGAG AACTTGGGAT TTGTAGTCGG TACGATTGTG TTTGCTTTAT	1020
TGCTCAACCC AAGTAATTTA CCTTCTTTAT TGATTATGAG AGGTATGTCG ACAGTTCTAT	1080
CTTGGACAGC CTACAAGACC CAACGTTTGG AAATGTCGAT CTTGCTTCAC ATGATTGTTA	1140
ATGGGATTGC TTTCTGTTTG TTGGCTCTTG TGGTGATTAT GAGTCGGACA TTAGGAATTT	1200
CTGTTTAAAA GTTTTATGT AGGAACCGAC CTCTTTCTAC CAGGGAAGA TGAATGCAAT	1260
CGTGCCATC TTTTCTTTT TATGGTAAAA TAGAAAAATA ATATGATGAA AATCCTTGAG	1320
GGAGTGACCG ATATGTCAAG TAAAGCCAAT CATGCAAAGA CAGTTATTTG CGGAATTATC	1380
AATGTAACCC CAGACTCCTT TTCGGACGGT GGTCAATTTT TTGCTCTTGA GCAGGCGCTC	1440
CAGCAGGCTC GTAAATTGAT AGCAGAAGGA GCCAGTATGC TAGATATCGG CGGAGAATCG	1500
ACTCGGCCGG GAAGTAGCTA TGTGTGAGATA GAAGAGGAAA TCCAGCGTGT TGTTCAGTG	1560
ATCAAAGCGA TTCGCAAGGA AAGTGATGTC CTCATCTCTA TTGATACTTG GAAGAGTCAA	1620
GTAGCAGAGG CTGCTTTGGC TGCTGGTGCC GATCTAGTCA ATGATATCAC TGGTCTTATG	1680
GGTGATGAGA AAATGGCTTA TGTGGTAGCT GAAGCGAGAG CGAAAGTGGT CATCATGTTT	1740
AACCCAGTTA TGGCTCGACC TCAGCATCCT AGTTCGCTTA TCTCCCTCA TTTTGGTTTT	1800
GGTCAAACCT TTACAGAAAA AGAGTTAGCT GACTTTGAAA CATTGCCAAT CGAAGACTTG	1860

1296

ATGGTGGCTT	TCTTTGAACG	AGCACTAGCG	AGAGCGGCAG	AAGCTGGTAT	TGCACCAGAA	1920
AATATCCTGT	TGGATCCAGG	AATTGGCTTT	GGTCTGACCA	AGAAAGAAAA	TCTGCTTCTT	1980
TTACGGGACC	TGGATAAACT	ACATCAGAAG	GGCTATCCAA	TCTTTCTCGG	AGTGTGCGGC	2040
AAGCgATTG	TCATCAATAT	CCTAGAGGAG	AATGGTTTTG	AAGTCAATCC	TGAGACAGAG	2100
CTTGCTTTCC	GAAATCGGGA	CACGGCTTCG	GCTCATGTAA	CTAGTATCGC	TGCCAGACAG	2160
GGTGTAGAAG	TGGTGCGCGT	GCATGACGTA	GCTAGTCACA	GGATGGCAGT	TGAAATTGCC	2220
TCTGCCATTG	GTCCTGGCTGA	TGAAGCGGAA	AATTTAGATT	TAAAACAATA	TAAATAAGAT	2280
GAAAGAAATT	GAAAACAATC	AGTGGATTGC	TAACACCGG	ACGGATCAAC	CGCATTTTGG	2340
CTTGGAACGA	ATGGTGGAAC	TGTTAGCTTT	CGGTGGCAAT	CCCCATCTCA	AACTCAAGGT	2400
CCTCCATATC	GGAGGGACTA	ACGGCAAGGG	CTCGACTATT	GCTTTTGTGA	AAAAGATGCT	2460
AGAAAAGCTA	GGGTTGAGAG	TTGGCGTGTT	TAGCTCGCCC	TATCTCATTC	ATTACACAGA	2520
CCAGATTAGC	ATCAATGGGG	AATCGATCTC	AGAAGCGAGG	CTAGAAGCTC	TCATGGCAGA	2580
CTATCAGTCT	TTGCTGGAGG	GAGAAGCGGT	CGCCAATTTA	CAGGGCACAA	CCGAGTTTGA	2640
GATTATCACA	GCCCTGGCCT	ATGACTACTT	TGCCTCAGAG	CAAGTAGATG	TGGCCATCAI	2700
GGAAGTTGGC	ATGGGTGGAC	TTTGGGATAG	TACCAATGTC	TGTCAGCCCA	TTTTCACAGG	2760
AATTACAAC	ATTGGCTTGG	ATCATGTGGC	TCTACTTGGT	GACACCTTGG	AGGTCATAGC	2820
AGAGCAGAAG	GCAGGTATTA	TCAAACAAGG	GATGCCCTTG	GTAACAGGGC	GTATTGCTCC	2880
AGAAGCCTTG	GCTGTGATTG	ACCGCATTGC	GGAAGGGAAA	GATGCGCCGA	GACTTGCCTA	2940
CGGGACAGAT	TATCAGGTTC	GTCATCAAGA	AAGTGTGGTG	ACAGGGGAAG	TCTTTGACTA	3000
TACAAGTGCT	GTCAGACAAG	GTCGCTTCCA	GACTAGCCTG	CTTGGTTTGT	ACCAAATAGA	3060
GAATGCTGGG	ATGGCCATAG	CTTTACTTGA	TACTTTTTGT	CAAGAAGATG	GTCGAGAGCT	3120
AGCAAGCAAT	GATTTTCTTG	GTCAAGCCTT	GGAAGAAACA	AGTTGGCCAG	GGCGTTTGGA	3180
AATCGTGTC	AGAGATCCCT	TGATGATTTT	GGATGGAGCC	CACAATCCCC	ATGCTATCAA	3240
GGCCTTGTTG	GTAACCTTGC	AAGAACGTTT	TGCGGATTAT	CATAAGGAAA	TCCTCTTCAC	3300
TTGTATCAAA	ACCAAGGCCT	TGGAGGATAT	GTTGGACTTG	CTGGGAGCCA	TGCCAGTTAC	3360
CGAGCTTACT	CTAACACATT	TTGCGGATAG	TCGGGCGACG	GATGAAAACG	TGCTGAAAGA	3420
GGCAGCTAAG	TCTAGAAATC	TCAGCTACCA	AGATTGGCAT	GATTTTCTAG	AGCAGAATTT	3480
GACAGATAAA	AAAGAAGAGA	AACAAACAGT	TAGGATTGTC	ACAGGTTCTT	TGTATTTCTT	3540
GAGCCAAGTG	AGGGCCTATC	TGATGGAGAG	GAAGAACGAG	AATGGATACA	CAAAAGATTG	3600
AAGCGGCTGT	AAAAATGATT	ATCGAGGCTG	TAGGAGAGGA	CGCTAATCGC	GAGGGCTTGC	3660

1297

AGGAAACACC	TGCTCGTGTA	GCCCGTATGT	ATCAAGAGAT	TTTTTCAGGT	CTTGGTCAAA	3720
CAGCAGAGGA	ACATTTGTCA	AAATCCTTTG	AAATTATTGA	CGATAATATG	GTGGTAGAAA	3780
AGGATATCTT	TTTCCATACC	ATGTGTGAAC	ACCACTTCTT	GCCATTTTAT	GGTAGAGCGC	3840
ACATTCGCTA	CATTCCAGAT	GGTCGTGTGG	CAGGCTTGTC	TAAGCTAGCC	CGTACGGTTG	3900
AAGTTTATTC	GAAAAAACCA	CAAATCAAG	AACGTTTGAA	TATCGAAGTG	GCCGATGCCT	3960
TGATGGACTA	TCTAGGTGCT	AAAGGAGCCT	TTGTTGTCAT	TGAGGCGGAA	CATATGTGTA	4020
TGAGTATGCG	TGGTGTAGA	AAACCAGGCA	CTGCAACCTT	GACGACAGTA	GCTCGTGGTC	4080
TATTTGAAAC	AGATAAGGAT	CTCCGTGACC	AAGCTTATCG	TTTAATGGGG	CTATAAAAAAG	4140
AATCCGCTTC	AAGCGGATTT	TTCTAGAAAG	GAATCATTAT	GGATCAACTG	CAGATTAAGG	4200
ATTTGGAAT	GTTTGCCCTAT	CATGGTCTTT	TTCTTAGTGA	GAAAGAATTG	GGGCAGAAAT	4260
TTGTCGTTC	AGCCATCCTA	TCCTATGATA	TGACCAAGGC	AGCTACAGAC	TTGGATTTAA	4320
CAGCCTCTGT	CCATTACGGA	GAATTGTGTC	AGCAGTGGAC	GACTTGGTFT	CAGGAAACGA	4380
GTGAAGATTT	GATTGAAACG	GTAGCCTATA	AACTGGTGA	ACGTACCTTT	GAGTTTATC	4440
CTCTTGCCA	AGAAATGAAG	TTGGAAGTGA	AAAAACCTTG	GGCACCGGTG	CATTTGTCAC	4500
TAGATACTTG	CTCGGTAACC	ATTCATCGCC	GCAAGCAACG	AGCCTTTATC	GCCCTAGGAA	4560
GCAATATGGG	AGATAAACAA	GCAAACTTGA	AGCAAGCCAT	TGACAAACTG	CGAGCTCGTG	4620
GCATCCATAT	TCTCAAAGAG	TCCAGTGTCT	TAGCGACGGA	GCCTTGGGGT	GGAGTGGAGC	4680
AGGATAGCTT	TGCCAATCAA	GTGGTTGAGG	TGGAAACCTG	GCTACCAGCA	CAAGACTTGT	4740
TAGAAACCTT	GTTAGCCATT	GAGTCAGAGC	TGGGACGGGT	GAGAGAAGTG	CATTGGGGAC	4800
CTCGTTTGAT	TGATTTGGAC	TTGCTCTTTG	TGGAGGACCA	GATCCTTTAT	ACAGACGACC	4860
TCATATTGCC	TCATCCTTAC	ATAGCGGAAC	GCCTTTTGTG	CCTTGAGTCT	TACAGGAAAT	4920
TGCGCCTCAT	TTTATCCATC	CGATATTAAA	ACAACCGATC	CGCAACTTGT	ATGATGCTTT	4980
GAAAAAATAG	AAAAACTCTA	GTTTTCAGTT	ACTTGCAACT	GAAGGCTAGA	GTTTTTATAC	5040
TCTTCGAAAA	TCTCTTCAAA	CCACGTCAGC	GTGCGCTTAC	CGTACTCAAG	TACAGCTTGC	5100
GGCTAGCTTC	CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	TAAAAAGGT	CATTTTCTTC	5160
TGGGAGGAGG	ATAGTTTCTC	TACCGTCCAT	GTCTAAAACC	AGTACTCTTG	GGGGATAACG	5220
AGGTCGAAA	GGATGGTTAA	AGTCAAAATC	AATGGCTGTA	GGGAGGTGTT	GACTTGAAAA	5280
GTGGAAGGTA	ATCTTTCCTT	GGTTATTAAG	CAATTGAAAC	TCGAGTTCTT	CTTCCAATTC	5340
AAAGACATTT	TTTAAGAAAT	GGTCGATGAT	ATACCAAAAA	GAGTCAATGA	TGTCATCAGG	5400

1298

CAAGCTGGTA ACAATACCAA AACTAGCAGA TCGCATGTGG GTATTGGTAA AAGCCATATC	5460
TCTGTCCCCT TTCTTTTCCC TTATCATACA GCAAATAGGA TTAAAAATCA AGAAAAGGTG	5520
ATTTTTTGAA AAGGATTTTA GTTACAGGGA GAAATAGGGA AAAAATTCCT AAAATCTAC	5580
CGAAGTTAAT AGGTAAATTC CCAAATTAAC TTGATTATAT AACTTTCAGT TACTTTGAGA	5640
AGTTACCGAA AAATATTTTT CATATCTATT GACTTTTAGG GGTAAAAATT GGTATGATAG	5700
TAGGCGGTAT TGTTTACCCC ATTTGAAAGG CCCCGGAACC TTCCAAATAC TTTTCGATGG	5760
GAAGGAACAC CCATCACCGT AAACAAAAAT CGAACTATAT ATAGGAGAAA TCATGAACAA	5820
AAACAACATTT ATGGCTAAAC CAGGCCAAGT TGAACGTAAA TGGTACGTAG TTGACGCAAC	5880
TGATGTACCA CTTGGACGTC TTTCTGCAGT AGTTGCTAGC GT	5922

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1988 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

TAACATCTA CGATGAGCTG TTGTGATTCT CATTAGTTCC CCTTCCCAA GAGGCATAGG	60
GGTGCGCATA ATAGATGTGC TCCTCAGAAA ATATATCAAA CAAGCGATTG AATCCGTTTC	120
CATTATCTGC CGTGATGGAA AGAATCTTGT GTTGTTTTAA GATGAGTTT AGAGCCTGAT	180
TGACCACCTC AGCACTTTTA TTTGGAATCA ATCGGATGAT CTGATGTCTA CTCTTTCGAT	240
CCGTCAAGAC AATCAAGCAG TAGTTTTTCG ATCTCGTAAG TAGAACCGTA TCAATCTCAT	300
AATGCCCATT CTCCAAGCGA AGATTGATAG CTTCAGGCCG CTGTTTCGATG GATTGACCAG	360
CAGGTTTAAA GTTGGTGCTA GCCTGTTTCT TAAGCGCTTT TCCTTTTCTA GGGTAAAGCA	420
AATCCTGCTT GCTTAACCCC AATTTTCCAT GATGAATCCA ATAGTAAATG GTTGAAATTC	480
CCACGTTAAC CCCTTTAGCC ATAACCATCA TTTCAGGCGA AAATTTTGG TTATGATAGT	540
GGAGAATCTT TTCCTTTAGT TCCTTGGTCA AGCTTGATTT CTTGACCGAG CGCTTGCGAT	600
TGTTTTCATA AGACTGTTGA GCGTAGTCGG CAGAATAAAC CTCTTTGAAG CGCCCTTTTC	660
CAAGACATTG TCGGACTGTC CCACGCTTGA TTTCAGTGTG ATAGTTTGAG GAGCTTTTCC	720
AAGTAGAGAG GCAATTTCTC TATTTGATTT TCCTTCTTTT TTCCATCTTT CGATTAAGCG	780
ACGGCTATCG ATTGTCAAAT GTTTGGCTTT TGTAATATAA TTGTCTTGCA TCTCTGTGCC	840
TTTCTTGTGT TTGTGGTTGA ACAACAAGTA TAACACAGAG GTGCTTTCTT ATGCCTACAA	900

1299

GAGCTTTCAT TATTTCCATT TTCTTTTGA TTTCACTCTA TTCTGAAAAA CTTGTGTATA	960
TTTACTGAAG CTAGCAAGTC TTACCTGTAA ATTTAATGAA AGCAACACAA AATCCGAGAG	1020
GGGAATCTCG GATTAATAGA TAGAGAGTTT TTAGTTTAAA TAAATTGTTT AAAATATCAA	1080
CAACATCACT TCTTTTCTTA ACCTGATAAG TCTTGATTCC TAATTTTGGG GCTACGATTA	1140
TATTGTCCTC AATATCGTCT AGAAAGACAC AATTTCCTAGG TTATAACTGG TATTTATCGA	1200
TAGTTACTCA TATACATCAG TCCACCTCCA TACTTATGTG CGAGCCTCTC TTTGTATTAT	1260
ACCTCCATAC TCACCTTACA GATTCTTTTG GTAATAATAT CTTTGCCTAA TGTAGAGACA	1320
GTCTTGCAAA GAAAAAATT CCTTGTAGCC ATGTTTCTGA TAAAAGTCCG GTGCCTGGAA	1380
CTGGTAAGTA TTGACAAAGG CAAAACAACA ATTTGATTC TTAGCTTCAC TTTCTGCCTG	1440
TTGCAATAGT TTTGAACCGA TTCCTTGCCC TCGCAGTTCC TCTTTTACAA ACAAATACTC	1500
GATTTCCTAGC CAATTCCAA AAGTCTCTGC TATCAAACCT GCCAGGAGAT TGCCCTTTTC	1560
ATCTTCGACA TAAAGATTAA GTGGCTCACT TTCAGCCTCT TCTCTTTTG AACGGTTATA	1620
AACACGAATC AGATTCCCTA TTTCTTGCGA TTTATGTGAT TCCTTATTTT CCAATCTAAA	1680
GTATAGTGAA ATGAAATAAA ACATGCGCAA ATCGATTAAG GAATTTAATC TAATTTCTAA	1740
CAATGTCTTA GAAATCAAAG TGTACTATTT TAACCTCAAT GCACTATACA TCTAATACTC	1800
AATAAAAAATC AAAGAGCAAA CTAGGAAACT AGCCGAGGT TGCTCAAAAC ACTGTTTGA	1860
GGTTGTAGAT AGAACTGACG AAGTCAGCTC AAAACATAGT TTTGAGGTTG TAGATGAAAC	1920
TGACGAAGTC GGCTCAAAAC ATGGTTTGA GGTGTAGAT GAAACTGACG AAGTCAGCTC	1980
AAAACAGG	1988

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 709 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

CCGGATATTT GTTTTATGTA ATTTTCTTGC AAGTTTCTTC TTAGTAGCTT GTCAGTCAGG	60
TTCTAATGGT TCTCAGTCTG CTGTGGATGC TATCAAACAA AAAGGGAAAT TAGTTGTGGC	120
AACCAGTCCT GACTATGCAC CCTTTGAATT TCAATCATTG GTTGATGGAA AGAACCAGGT	180
AGTCGGTGCA GACATCGACA TGGCTCAGGC TATCGCTGAT GAACTTGGGC TTAAGTTGGA	240

1300

AATCTCAAGC ATGAGTTTGT ACAATGTTTT GACCAGTCTT CAAACTGGTA AGGCTGACCT	300
AGCAGTTGCA GGAAATTAGTG CTACTGACGA GAGAAAAGAA GTCTTTGATT TTTCAATCCC	360
ATACTATGAA AACAAGATTA GTTCTTGGT TCGTAAGGCT GATGTGGAAA AATACAAGGA	420
TTTAACTAGC CTAGAAAGTG CTAATATTGC AGCCCCAAAA GGGACTGTTC CAGAATCAAT	480
GGTCAAGGAA CAATTGCCAA AAGTTCAATT AACTTCCCTA ACTAATATCG GTGAAGCAGT	540
CAATGAATTG CAGGCTGGAA AAATAGATGC TGTTCATATG GATGAGCCTG TTGCACTTAG	600
TTATGCTGCT AAAAACGCTG GCTTAGCTGT CGCAACTGTC AGCTTGAAGA TGAAGGACGG	660
CGACGCCAAT GCCGyTGCTC TTAGAAaATA GTGATGATTT GAAAGAAGT	709

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1680 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

TATAAAATGT TAAGTTAAAT GATTTCAAAA TTCAGAAAGG GATTGCTTTA TGCAGTTCCT	60
TTTTATTTTA ACAGGAGTGA AACTATAGTG TTTCTAAATT GTGAATCAAT CAAAAGTAT	120
TGTGATGGGG CTATTCTAGC TTTAGAAACC TTCAAAAATT AAAATTTAAG GCAATCAATT	180
ACTTGGAAGA GTATGAAAGC ATTTAGTTTA TAGGAATTCT AGGTCTAGAA TTACATATAT	240
ATATTTATGA AGACGGGGTG TTCGATAGTT AGTATTGTTC TATTCTGAAA GATTTGAGCT	300
GTCAGTTGTA TAGAAAGTGT TCGAATTTTT TTAAGTGATT AAATTAGTTA ATTGTATGAG	360
GTGCTTTATG ATATAATGTT CTTAATGAAT TTCAGAAAG GAAAACCTCA AATTGTTCTA	420
CAAATTTCTA CTCTTCGACC TCGACCACAC TCCTCTTGAT TTTGATGCTG CTGAGGATGT	480
GGCTTTGACC CAACTTCTAA AAGAAGAAGG ACTTCCGGAT ATTCAGGCTT ATAAAGATTA	540
TTACGTTCCCT ATGAACAAGG CTCTCTGGAA AGACTTGAG CTGAAGAAAA TCAGTAAACA	600
AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT TTTGGACAGG AAAAAGACGG	660
TAGTTTCTTT GCCCAGCGTT ACCAATTTTA CCTCGCCCAG CAGGGACAAA CACTATCGGG	720
CGCTCATGAT CTCTTGACA GCCTCATTGA GCGTGATTAT AACTTGATG CTGCGACAAA	780
TGGCATTACT GCCATTGAGA CAGGACGTTT GGCTCAATCT GGTCTAGCAC CTTATTTCAA	840
TCAAGTCTTT ATCTCAGAAC AGTTGCAAAC TCAAAAGCCG GATGCTCTTT TTTATGAAAA	900
GATTGGCCAG CAAATTGCTG GATTTAGTAA AGAAAAGACG CTGATGATTG GAGATTCTCT	960

1301

AACCGCCGAC ATTCAAGGTG GCAATAATGC GGGGATTGAC ACTATCTGGT ATAATCCTCA	1020
TCACCTCGAA AATCACACAC AAGCCCAGCC GACTTACGAA GTCTATTCTT ACCAAGACTT	1080
GCTGGATTGT TTAGATAAAA ATATCTTTGA AAAGATCACA TTTTAAAGGA GACGAGCTAA	1140
TGACTACAAA AAAGCTAATA TTAATATTGA AGACTACATT GAAATGTCTG AAGTTGATTT	1200
TAATGAAGCT GTTAATTATG AATTACATC TGACACTTGT CAATTAGCAA ATAGTATTTA	1260
TCAATCTCTT TTTAAGTTT TTGATAAGAA AAATTTCTCT GCGGATTAA TTTTACTTG	1320
GAAATCTCCA TCATTAGTCA AAGAAGGGGA TTATATTGGG AGAAGGGATT CACAAGTAGA	1380
TAATCTTAGA GTAATAGGAA ATATATTTCC GAATATCTT ACTAATCGAA AATATAGCCT	1440
CAATATGAAT CGTAATGGCT GTATGGGAGA TTTTCCTCAT GACTTTTTTG ATATATACCT	1500
AGATCATGTA GCAAAATATG CCTACGAACA AAAAGTTAAT AATATTAAAG AGTATTATCC	1560
TTTAAAAAGA GCGATTTTAC ACCAAGAGAA TGCATTGTAT TTTTCGATTT TTTCTAATTT	1620
TGACGACTTT TTAGAAAAAA ATTATTTAAA GACTATATGG CAAGTTTCTA AAGAACTCC	1680

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 598 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

AGCTCGGTAC GTAGTATnTG TGGTGCATAA ATGAGTGAAA AGAGGATAGA GAGGATGAGG	60
CCGATAAGAA CACCGGTAGC TGCATCGTGA AATACTTGTT TTTTCATAGT TCTAATTCT	120
CCTTGATGGT TTTTAGATAA CGGCGTGAAG AGTAGGTGAA GCTTTCGTTT TTCAAGAAAA	180
TTTCTACCAG ACCGTTTGGC GTGAgCTTGA GGTGAGAGAT GGAATCGATA TTGATGATTT	240
CTGATTGGGA AATTGGGATA AAATTGGTTG GCAAGAGTTT AAGAACCCTGA TAGAGTCGCA	300
AATCAATGCT GTAGGTCTGA CTCGCGGTTT CTGCTAGAAC CTTCGATTC TCGATATAGA	360
AGCGCTGAAT CTTGCCAATC TCAACTAGAT AGACCTGATC ATCGATTTT CCTTGATTT	420
TTTCTCTTTG GTCCAGATTT TCTGCGAACT CGATGACTTT CTGGACTTTT TCGGTTTCTT	480
GAGGTGCTTG GACAATCAGC TTTTCCTCCT CGTAAGTCTC ACTAATCTGT AGTTCTACTT	540
TCATAGTTT CTCTCCTTT CAGTTATACA AGGTTGTGAT CACTTCCTGT ATATCCGG	598

(2) INFORMATION FOR SEQ ID NO: 272:



1302

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1099 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

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CCAGCAAATC AATAACTGCA ATTGCTATAA AATGGATTCT ATAGAGTTT TTCATGACAA      60
GACCTCCCTC TTTTATCTAA CTTCATTCTA CTCCAAAAGA ATGGGAGTTA CAACTAAAAT      120
GATAAAAATA GCAGAAGGGA GATTCTCTTA AGTTGGCTAG TATTCTTTAT TTGAGTTTCC      180
TTCTATTATC TAACTTCTTC ATCATTCCAG ACAATAAAG CTCGGATTGC ATTGAGGATA      240
TAAAGATGT ATTTACCGAT ATTGGCGAAG TTTCTTGAA TACCAGCTT TGTCAGCTGA      300
ACGAAATTGT AAATCAACCA AAAGCCCAC TGAGTTGTTA GTTTTAATGC ATTCAAAGCA      360
TTGGCAATGA GGGACAGTGC AAAGGCAATA GTTGTTACGT AGGCAAGGAC ATTCATCTTG      420
CCCCCATATC CGATATAGTT GGTACAAAAG GCAAAGAGGA AGGCGATGAT GGAAATGATG      480
ATGGCCGCCA ATTTTACCTG TTTTGGCTC ATTTGGTTGG GTCTGCCTTC TTGCGAAGCT      540
TCCCACTTCT TTATAGCAA GGTATAAATG AGGAAGGTGA CGGGATAGGT AATGATGGCC      600
GCCTTATTTC CAAGGATATA ATCAATAGCA CCGGACAAAA TGGTATTAAC AATACCAAAG      660
TAATTTCCCC ATTTGCTTAA TTTCCCGTG AAACGAGTGG ACAACATGGA AATCCAACG      720
TTGTTACGG AAATCAATCC AAAGGTACA AGAGCTGTCC ATGATCCCCA GTCTACAAAT      780
TTATCGAGGT GTGAGTTGAG GTAACCAGAT GCAATCGCAA TCCAACGAC CAAAGCAACC      840
CCGAAGAGGT CAACTATTT AGATGTAGCA AAAATTTTA GTGATTTTTT CATAGGTAA      900
ACTACCTTTC TTTTTTCAA ATATTCTCCC ACCAAATGAA AGTAAAATAA AATGATAGAA      960
ATAAACCCCT GAAAAATAAG GTTCTATAAT ATTGTAGTG GGTAAATCCA CTATAGATAT      1020
TATGGAGCCT ATTTTATTGT AGAAAAAAG TCCCATATGA CCTATAATGA AAAGCGACAA      1080
AACAACTCAT TAGAAAGAT                                     1099
  
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(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2723 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

1303

CTGGGATTCA CGTGAAAAGG AAGCCCAGAG AGTAGCCAGG TGTACTGCTA GAACAGTGAG	60
TGAAATTGAA TATTACCATA GAGAGTCAAC CCAGATAGCT CAGGCTTTAC TTGAAAATCA	120
AGCTCGTATC GAGGGAATCT ATAAATACTT TAGCCTTAGC ATGCCAGACT ATTTTACTG	180
GCAATTAGAG CGGAAAGCTT CGCCTTATAT ATCAGTCTCT CTGTATGAAA ATGTTGATGA	240
CCTCTATGTT CGAAATGATT TTGTAACTGG GGTGGCCATT GCTTTTCAAG ATTACAAGGA	300
AGTCTATGTT TCTACTAAAG ACAAACGTAG GkkAGAAAAA ATCAGGGCTG AGGATTTCAA	360
ACCAGCAGGA AATAGTTTTG CCATTCCAGT GTCAGATCCA GTGTCAGATC AAGACTTAGG	420
AGTGATTTAC ATCTCCTTGG ATCCTGCTGT TTTATACCAT GCCATTGATA ATACTAGAGG	480
TCATACTCCG ATGGCAGTAA CAGTGACCTC ACCTTTTGAT ACGGAGATTT TTCATATGGG	540
TGAGACAGTT GATAAGGAGA GTGAAAATTG GCTAGTTGGC TTAACCTCTC ATGGATATCA	600
GGTTCAGGTG GCAGTTCCTA AAAACTTTGT TTTACAAGGA ACAGTGACTA GCTCTGCTTT	660
GATTGTGGGT TTGAGCCTTC TCTTTATGT CATTCCTTAT CTGACTTTGA GGCAGACTTT	720
TGCTAATTAC CAAAAGCAGG TACTGGATTT AGTAGAATCC ATTCAAGTCA TTGCTCAAGG	780
CGAAGAGGGG CGTCGGATTG ACATTTCCGA GAAAGATCAG GAATTACTCC TAATCGCGGA	840
GACGACCAAT GATATGTTGG ATCGATTGGA AAAGAATATC CATGATATTT ACCAGTTAGA	900
GCTTAGTCAA AAAGATGCCA ATATGCGAGC CTTGCAGGCG CAAATCAATC CTCATTTTAT	960
GTATAATACG CTGGAGTTCT TGCGCATGTA TGCAGTTATG CAGAGTCAAG ATGAGTTGGC	1020
AGATATCATT TATGAATTCA GTAGTCTCTT GCGTAACAAT ATTTCCGACG AAAGAGAGAC	1080
CCTCCTCAA CAGGAATTAG AATTTTGCCG TAAATACAGC TATCTCTGCA TGGTTCGCTA	1140
TCCAAGTCC ATTGCCATAG GTTCAAGAT AGATCCAGAG TTAGAGAATA TGAAGATTCC	1200
CAAGTTTACC TTGCAACCGC TGGTAGAAAA CTATTTCCG CATGGTGTG ACCACAGGCG	1260
GACAGATAAT GTGATTAGCA TCAAGGCTCT TAAACAGGAT GGTTTTGTGG AAATTTTGGT	1320
GGTCGATAAT GGTAGAGGAA TGTCGGCTGA AAAGTTGGCA AATATCCGAG AAAAATTAAG	1380
TCAGAGATAT TTTGAACACC AAGCCAGCTA CAGTGATCAA AGGCAGTCTA TCGGGATTGT	1440
CAATGTACAC GAGCCTTTTG TGCTCTATTT TGGAGACCGC TATGCCATTA CTATAGAGTC	1500
TGCAGAGCAA GCCGGTGTTC AGTATCGTAT TACAATTCAA GATGAGTAGA AAGGGAGAAA	1560
ATGTATAAAG TATTATTAGT AGATGATGAG TACATGGTGA CAGAAGGTCT GAAGCGTTTG	1620
ATTCCCTTTG ATAAGTGGGA TATGGAGGTC GTCGCAACAG CCAGTCATGC CGATGAAGCT	1680
CTAGAATATG TTCAGGAAAA TCCTGTCGAT GTCATCATTT CCGATGTCAA TATGCCAGAC	1740

1304

AAAACAGGGC TTGATATGAT TCGGGAGATG AAAGAGATCT TACCAGATGC TGCCTATATC	1800
CTGCTCTCAG GTTATCAGGA GTTTGATTAT GTAAAAAGAG CAATGAACCT TAGTGTGGTG	1860
GA CTATTTGG TCAAGCCTGT TGATAAGGTA GAGCTGGGAA ATCTGCTGGA GAAGATTGCA	1920
GGTCAGCTCG GCGAGAGAGG GAAGAAAAGT CAGACTCTTA GTCAAGAATT AGACGAGGCT	1980
GGATTTGTTA GTTATTTAGG GGATAAGGAG AATTGGTGGA TAGGTCTATC CAAGGAAAAA	2040
CAAGGTTCCCT TCACCATTCC CTACTATGTC TTGGGTCAAG ACTGGCAGAT TTTCATTTCT	2100
GGCCACCCCC TAGATGGTTT AGTCGTTACA CCTTTTGAAG CTCCTTATCA AGAACACTTT	2160
GAACGCTGGA AGCTGAATGC TGAGAAAACC CTCTTTTACG GTTCTGTAAA TCTGCAGCAG	2220
TCTGAGAGTC TCTTTGCC TAACGAACCG ATTTATAGGG TTATCATTCA GGGAAATCTC	2280
AA TCAAAATCG TAGAAGAGTT AAATCTCTTG GAGAAGGTAG TTCTTGAAAA TACACCTCGT	2340
GT TTCGATTA CTAACAGCT TTTTATCCAG TTTGTCATGG ATGTTTCCA TTTATTTGAA	2400
CATCTCAAAG CTGATGATAT GACGGACATT GTCAAAACCA TTCATGCTAT TCAATCCTTC	2460
GATGAATTGG TTTCTTATAT CAAGGAAACT CTGATCAGCT TTTCCGTCAT ATACCGTATG	2520
AATGAAAATG TGGTCAGTGT GCTGGAAGTC ATTGGTCGTG ATTACCAAAA AGAGCTTTCC	2580
CTCAAGGATA TCAGTAAGGC CCTCTTTATC AATCCTGTCT ATCTAGGGCA GTTGATTAAG	2640
CGTGAAACCG ATTCGACCTT TGCAGAGTTA CTAAACAAAC AACGTATTAA GGCTGCCCAG	2700
CAGCTCTTGC TTTCAACTAG TGA	2723

## (2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 836 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CCGCAGTTTT TTAAACCGT ATATAAGTAT AGCATAGTCA AAAAAAGAAT GCAAGATTTT	60
TGCAAACTTT TTTAAATTT TTCGTAATTT TTCTTTTAAA GTTCTACTGT CAGGACTTGA	120
CCTTGCTTAA CAACCTGTTC TCCGGCGATA TAAACATCAT CTACATCACT AGATTAACT	180
GCATAAACCA GGTGAGACAG CATATTTTCC TGAGGTTGGA GATGAATTTT CCCTTGTTGGT	240
TGAATGACCA GAAAATCTGC TTGCTTGCCG ACTTCCAGAC TTCCTATCTG ATTTTCCATT	300
CCAAGGACCT TAGCCCCTTC GATTGTCAGT ACCTTGAGAG CTGTTTCGAT TGGAACTGG	360
CTGGCATCCC CACTTTTCAT CTTCTGAAGA AGAGCTGCAG TCCTTCCTTC CTCAACATA	420

1305

TCTAGATTGT TATTGGAAGC AACCGAGTCA GTCGCAATTC CGACTGCTAC TCCCGCTTTT	480
TGGAGCTGGA TAATTGGAGC AATTCCTGAT CCCAGTTTGA GGTACTGAT AGGATTGTGG	540
GCGATAGChA CTTGAGAAGA TGCCAAGCGT TCAATTTCTC TCTCGTTTAA TTCGACCCCG	600
TGAGCAAATA CGGACGGATG ATCTAAATAA CCCAGTTCTT CAAGAAAAGC AAGGGGGCGT	660
TTGCCGTATC GTTTGAGGAT AATTCCTGAC TCCTCCTTGG TCTCCGCCAC ATGGACATGG	720
AGCGGAATAT TTAGCTCTTT TGCCATTTC AACTCGCTT CCAGCAAGTC TCTACTGCAG	780
CTATACGGAG AATGAGGTGC TACCATAACC TTGAAATTG GATTTTATA TTTTAA	836

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2335 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ATTTTATTTT ACTTTT TAGG TGGTCTGGGG CTATTCCTAT ATAGChTCAA GACCATGGGA	50
GACGTTTAC AACAGCTGC TGGAGATCGC CTGGGTTTTT ACATTGACAA ATATACTAGT	120
AATCCTTGT TTGGAGTTCT GGTTGGTATT GGGATGACTG CTCFAATTCA GTCTAGTTCT	180
GGTGTACAG TTATCACAGT CGGCCTGGTC AGTGCCGGTC TCTTAACCTT ACGTCAGGCT	240
ATCGGGATTG TCATGGGTGC TAATATTGGG ACAACTGTCA CATCCTTTCT CATCGGTTTT	300
AAATTAGGTA ACTATGCCCT ACCTATGCTC TTTATCGGTG CCGTCTGTCT TTTTTTTACG	360
AAAAATCGGA CAGTCAATAA TATCGGACGC ATCCTCCTTG GTGTCGGTGG TATCTTTTTT	420
GCCCTCAATC TCATGAGCGG CGCAATGGCT CCACTCAAGG ATTTACAGGT CTTTAAGGAC	480
TATATGATTG AGCTAAGTAA GAATCCTGTT TTGGGTCTCT TTGTCCGTAC TGGCTTGACC	540
TTGCTAATTC AAGCTTCTTC GGCTACCATT GGGATTTTAC AAAACCTCTA CGCCGGCAAT	600
CTAATTGATC TACAGGGAGC TTGCCAGTT CTATTTGGTG ACAATATCGG GACAACCATT	660
ACAGCCATCA TTGCCTCTTT AGGGGCTAAT ATTGCAGCTA AACGGGTAGC AGGAGCTCAT	720
GTGCTTCA ACGTTATCGG AACAGTTGTC TGCCTTATTT TTCTAGTTCC TTTTACTGTC	780
CTGATTCATT GGTTTGAAGC TACGCTAAAT CTAGCACCGG AAATGACCAT CGCCTTTGCT	840
CACGGAACCT TTAATATTAC CAACACCATT GTCCAATTC CATTTATCGG AGCTCTGGCT	900
TACTTTGTAA CCAAGATTAT TCCTGGAGAG GACGAGGTG TCAAATACGA ACCCTTATAT	960

1306

CTTGATGAAC ATTTTCATCAA ACAGGCCCCA TCTATCGCTC TAGGAAATGC TAAGAAAGAG	1020
CTCTTGCACT TAGGAAACTA CGCTGCTAAA GCCTTTGACC TTTCCTATAA GTACATCATT	1080
GACTTGGATG AAAAAGTTGC TGA AAAAGGG CATAAAACCG AAGAAGCAAT TAACACCATC	1140
GATGAGCAAT TAACACGTTA TCTCATTTGCC CTTTCAAGCG AAGCTCTCAG CAAAAAGAA	1200
AGTGAAGTGC TTACCAATAT CCTTGATTCC TCCCCTGATT TGGAACGGAT TGGAGACCAC	1260
ACGGAGGCTC TACTCAATCT GACTGACTAT CTTCAACGGA AAAATGTTGA ATTTTCTGAT	1320
GCCGCCTTGA AAGAATTAGA GGAAGTTTAC CGCCAAACTA GTGACTTTAT CAAAGATGCT	1380
CTGGATAGTG TGGAAAACAA TGATATTGAA AAAGCACGCA GTCTTGTTAGA ACGTCATGAA	1440
GCAATCAATA AGATAGAACG TGTTCCTCAGA AAAACCCACA TCAAACGCCT CAACAAAGGC	1500
GAATGTTCAA CACAAGCTGG GGTCAACTTT ATCGACATCA TCTCACACTA CACTCGTGTA	1560
TCAGACCACG CTATGAACCT TGCTGAAAAG GTTTTTCAG AACAAATCTA AGAACCAAGA	1620
AGCTATCCAT CATAATTGGA TGGCTTTTTA CTTTTTCCTA AGCAAGACTA GGATGAATGA	1680
AACTGAAAGA GTATTCTGCA GATATATAGT CCCCAATTAT TCACCCCAA TCTAAAAACC	1740
ATCCAGAATC CTGCTTAG CTTAGATCCT GGATGGTTTC TTTTTCACC CAATGGGTGT	1800
TTTTTACTAG ACAAAAAAGA GTTCCCTT TATGGTATAA GTGTAGAAAA AAACACAAAA	1860
AGAAAGGAAA CTCACATGAA CAGTTTACCA AATCATCACT TCCAAAACAA GTCTTTTAC	1920
CAACTATCTT TCGATGGAGG TCATTTAACC CAGTATGGTG GTCTTATCTT TTTTCAGGAA	1980
CTTTTTTCCC AGTTGAAACT AAAAGAGCGG ATTTCTAAGT ATTTAGTAAC GAATGACCAA	2040
CGCCGCTACT GTCGTATTTC GGATTCAGAT ATCCTTGTC AGTTCTCTCT TCAACTGTTA	2100
ACAGGTTATG GAACGGACTA TGCTTGTAAG GAATTGTCAG CTGATGCCTA CTTTCCAAAA	2160
TTGTTGGAAG GAGGGCAGCT TGCTTCACAG CCAACCTTAT CCCGTTTTCT TTCCAGAACT	2220
GACGAGGAAA CAGTCCATAG TTTGCGATGC CTCAACCTTG AATgKCGAA TTCTTTTAc	2280
AGTTTCACCA GCTAAACCAA CTCATTGTAG ATATCGATTC TACCCATTTC ACAAC	2335

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 752 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CGGATTCACT GTTGTGACT AATCAATAAC ACAGTAGAAA ATCTCACAGC AGTCTATTAG	60
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1307

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TTGCTTTTCA TACTAGGCAA GTGACTGAGG CTTGTACTTG GGTACAGCAA GGGAGCTTAA      120
GGCCGTAGAA GAGAAAAATA GTAGACTGAA AACCCGCAAG ACTTCATCAT TTCGAGAAGT      180
GACGTGGGAG ATGAAAATCG ATTGAACCAC TTACAAGGAG AATAGAAAAT GGCTAAAAAA      240
AGCAAACAAC TTCGTGCTGC TCTTGAGAAA ATCGACAGCA CAAAAGCATA CAGTGTAGAA      300
GAAGCTGTAG CACTTGCAAA AGAACTAAC TTTGCAAAAT TTGATGCAAC TGTAAGATT      360
GCTTACAAC TGAACATCGA CGTTAAAAAA GCTGACCAAC AAATCCGTGG AGCAATGGTA      420
TTGCCAAACG GTACTGGTAA AACTTCACGT GTTCTTGTTT TCGCACGTGG TGCAAAAGCT      480
GAAGAAGCAA AAGCTGCTGG TGCAGACTTT GTTGGTGAAG ATGACCTTGT TGCTAAAATC      540
AACGACGGTT GGTGGACTT CGACGTAGtT ATCGCTACAC CTGATATGAT GGCTCTTGTT      600
GGACGTCTTG GACGTGTCCT TGGACCACGT AACTTGATGC CAAACCCTAA AACTGGTACT      660
GTAACAATGG ATGTTGGCAA AGCGGTTGAA GAGTCTAAAG GTGGTAAAAA CACTTACCGT      720
GCTGACCGTG CAGGTAACGT TCAAGCAATC AT                                     752

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(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2643 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

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GTCAACATTG ATTTCAAGGC TGTTTGCTTT CTATCTCCCC TTTTTCATAA TGTATAATAA      60
AATGAAATAA TAACAGGACG AATTGATCGG GACAGTCAA TCGATTCTA ACAATGTTTT      120
AGAAGTAGAG GTGTACTATT CTAGTTTCAA TCTACTATAT TTTCGTACAG GTGCTTCAAC      180
CATTTGAACG ATTTCAAATC CTTCTTTTGG GTAAAGATTC TGAGCTCTTT GATTTCCTC      240
GAAGACATTT AGAGAAATAC TGTCTATATC TCTATTTTCA AATGCTAAAC TAACAAATTT      300
CCTTAAAGCC TTGCTACCTA AGCCTTGCTC CTGTTCTGG GGGTTGATAA AAAATCTCCC      360
GATATGAAGA TTGCTGTCTT CTAGCCTGAT TTTCTGGATA AATCCACAA ACTCTTGTTT      420
ATCAAAGATT GAAAAGACTC CTTCCAAGGC TTGAAGTGTC AGTAGAAAAG GAATCCTTGG      480
TCCCATCCAT TGTCTTGAA AGGATTTGCC TAGGGAGTTG GACCACTGGC ATACAAATTG      540
AGCGTTTTCT GTGCTCACCT TTTCTTCAA ACGAATTGTC ATCTTTTCCT CACCACCTTA      600
TCTATGTTTC TCCATTATAC TATTTCTCCC ATTTTTTACG AATAGATAAG TATGATTGAT      660

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1308

TTTTATTTT TTCTCGTCGG GAGCATTCTA GCTTCCTTTC TTGGTTTGGT CATTGACCGT	720
TTTCCAGAGC AATCCATTAT CAGTTCAGCC AGTCACTGCG ATTCCTGTCA GACTCCCTTG	780
CGTCCCTTAG ATTTGATTCC GATTCTCTCA CAGGTCTTCA ATCGCTTTTCG CTGTCGCTAC	840
TGCAAAGTTC GCTATCCTGT CTGGTATGCC CTCTTTGAAT TAAGCTTAGG ACTCCTCTTT	900
CTGCTTTACT CTTGGGGATG GCTCTCCTTG GGGCAAGTCG TCCTAATCAC CGCTGGTTTG	960
ACCTTGGGTA TCTACGACTT TCACCATCAG GAATATCCCT TACTGGTCTG GATGACTTTC	1020
CAGCTAATCC TAATAGCTTC CTCTGGCTGG AATCTGGTCA TGGTCTCCTT CCTCATACTT	1080
GGAATTTTGG CTCATTTTAT CGATATCCGC ATGGGTGCAG GGGATTTCCCT CTTTTTAGCT	1140
TCTTGTGCTC TCGTCTTTAG CGTAACGGAG TTACTGATCT TGATTCAGTT CGCTTCTGCG	1200
ACGGGTATCC TGGCCTTTCT CCTGCAAAAG AAAAAGGAAA GACTTCCTTT CGTGCCTTTC	1260
CTCTTACTTG CTACTTGTTC GATTATTTT GGTAAAGCTAC TGCTTGTCTG ATAAAATCCA	1320
ATTCTGCCA TATATCCTTC ATGAAATTAT TTCACAGTCA AATTATAAAT TATTTCTTTT	1380
GTACAAAGGG ATGATGTTAT CAAATCGATC TGTCTTCTA TCTTCTTGAT ACTGATCAAA	1440
AAATTTTCAAT TCGACTGAAA ATATTTTCGCT TATAAACTGT AAACGAATAC TTTGTTTAGA	1500
CATTATAGTC GCTAGACTGA CTAGATGATT ACTCAAAACG ACGTCCAGAA TACTCTTTAC	1560
TTTGCTTGGT TTTTAAACAA AAATTTGATC ATCCAAGGGT TCAATCATTT TGTAACCTTT	1620
TTGCGCAATT TGACGATAAA AGTAAGAATG TTGCTTTGGA GTCAATAATC CTAACCTAAA	1680
AGCTCGATAC TCTAAAGCCT GTATCGAAAC ATTCAAATCC GACTTCAATA AAATATAACT	1740
ATCAGGATTG CTGACACGCT TGCCAACCCT CTCTTCAAAT TTGACTAAAA ACTCTTCTTT	1800
TGGCAATAAA AAACATGATG CAAAATAATT TGCTTCTTGC TCCAAACGAT CGCCATCTTC	1860
ATTCATATCT TTATATTTAT GTAAAAGAAT ATGTCCTAGC TCATGAGCTA AGTCAAAATT	1920
TCGACGTACA GATGATTTAT TCGTTCCTAA CACAATATAA GGTCTTCCCA ATTTTGACCA	1980
TGCGCTATAA GCATCAGCTT GGCCATTAAT TAATCGTTCC ACGATATAGA TGCTGAACG	2040
TTCTAATTTA TAAAGCAAAT CATGATTATC TTTTGAAATA CCTAATTTTT CCCTGGCATA	2100
AAGAGCCAAT TCCTCAATGG ATTCTCCCTT ATGATAAGAT TCACTCACTA CATTACTTAG	2160
GTCAATGAAT ATAATATTAG GTATAATTAC AAACTTTCA AAATAATCAA TCAAACTATC	2220
TACCTTATGT AAATACATAG TTGAATATC TATTTGTTTC CGTGTGCTA GGTCTGCATT	2280
TCTAAAGGCA ATTACAGAAG AATCAATCG AATGCTCTCT TCTTCCTGTT CAAAATAAGT	2340
TAAATCAACA TGAAATTGGT TGGCCAAATG CATTTTGGTT GATAATTTAG GTTTCGTTTC	2400
GTGACTCA AACTGCCAAA TGGCTTGTTC CGTTAAATTA ATTCTCTGAG CTAATCTGCG	2460

1309

TCTACTTAAA CCATTTAACA GCCGTAATTC TTTCAATACC CGACCATTAA ACATTTACAT 2520  
ACTCCTTACT ACTTTTGACC TTCTTGTTTT TCTATTCTTG GAATAATTTC AAAATCTTCT 2580  
GTTTCCGATA ATTCTGAAAA ATTAGGAATA TCTTGATATT TAGCTTCTTC GAAATGGTAC 2640  
GGG 2643

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 582 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

TGACCAGTGG CAAATGGCT ATCCAAATGC AGATGTTATT ATCGATGATA TCATCTCAGG 60  
GCAAGCCTAC GTAGCCTTGG AAGAGGGAGA ACTGCTAGCC TATGCTGCTG TGACCAAGAG 120  
TCCAGAGGAG GCCTATGAAG CTATTTATGA GGGAAACTGG CAAGCTGGAG AGTCAGAGTA 180  
TCTAGTCTTT CACCGTATTG CTGTGGCAGC AGATCTGCAG GGAAaAGGAG TTGCTCAAAC 240  
CTTCTTAGAG GGCTTGATTG AAGGTTTGA TTATCTTGAT TTTCGCTCAG ATACGCATGC 300  
TGAAAAACAAG GTTATGCAAC ATATTTTGA AAAACTTGGT TTAAACAAG TCGGTAAGAT 360  
GCCAGTAGAT GGCGAACGCT TGGCCTATCA AAAATTAAG AAATAATGCA AAAGAAGTAT 420  
GTAAAAATCC TCTACTCCTC ACCAATTGGT ATTCTATCAC TTGTAGCTGA TGACCATTAT 480  
TTGTATGGAA TTTGGGTTCA GGAGCAGAAG CATTTTGAGA GGGGACTAGG AGATGAAACG 540  
ATAGAAGAAG TTCTwAGTCA TCCTATTTTA GACCCAGTTA TT 582

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 554 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

CCCAAGCTAC TAAGAGACTA AAAGTTGCTA GAGAAGCAAG AGAAAGTGTG AATCTTTTTA 60  
ATTCATGAT GAATTTCCTT TCTGCTACCA ATTTAGAGAA ATTTTCTCTA ACCAGCAATT 120  
CCCCTAGTAT AACAAGTTCA AAAAATGGAG TCAATTTATC TGCTCACGGT CCAGCAGGTA 180



1310

GCCCCGTACT TCTGAGATAA AATAGAGAGA CCCTGTAACG AACAGCAAGT CTTGAGCGTC	240
TGCCCTTTCT TCAAAATCGC TGATAAATTC TCGGTAAGAA GAAACTATAT CGTAACCTGT	300
CACATCCCTT TCGTCCAAAG CCCCTGATA GTCAAAGCCG GTCACCTTGA GTTCCACCTG	360
AGGCAATTTT TCAGTCAGAT AACCCAACAT CCCTTGATAA TCCTTACGTT TCAAGGATCC	420
AAAGAGGATT TGAGGTCGAT AGCCTTCCTG CTCTTTTCTT TTGATAAACT CAGCCAAGCG	480
AGTCAAGGCA GGGAGGTTAT GAGCACCATC CAAATAAATC TGTGGGCGAA TACGCTCCAA	540
GCGAsCAGCC CAAT	554

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 766 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

CCGGTTTTTC AAATGAATTT CTTGGTTGTG GCTAAAAAT ATGCTACACT ATCAATATGA	60
AAATTTTAAT CCCAACAGCA AAAGAAATGA ACACAGACTT CCCAAGTATC GAGGCAATTC	120
CTTTAAACC AGAAAGTCAG GCCGTGCTTG ATGCCTTGGC TCTCTATTCT GCCAGTCAAT	180
TGGAGAGTTT CTACAAGGTA TCAGCTGAGA AAGCGCGGA AGAATTTCAA AATATCCAAG	240
CTTTGAAAAG GCAAACTGCT CAACACTATC CAGCCTTGAA ACTTTTGAT GGGCTTATGT	300
ACCGCAACAT TAAGAGAGAT AAGCTGACCG AGGCGGAACA AGATTATCTT GAAAATCATG	360
TTTTCAATTAC CTCGGCTTTG TACGGTGTG TTCCAGTCTT GTCACCCATG GCTCCTCACC	420
GTTTGGAATTT TTTGATGAAA TTAAAAGTCG CTGGTAAGAC TTTGAAGAGC CATTGGAAGG	480
CAGCCTATGA TGAAACTCTG AAGAAGGAAG AAGTGATTTT CTCTCTCTTC TCATCAGAGT	540
TTGAGACTGT ATTTTCTAAG GAAATCAGAG CAAAGATGGT GACCTTCAA TTCATGGAGG	600
ATAGAGGCGG TCAGCTGAAG ATTCACTCAA CTATCTCCAA GAAAGCGCGC GGGGCCTTTC	660
TAACAGCTTT AATAGAAAAT CAAGTACAAA CTGTGGGGGa AGCACGTCGC TTGAACTTTG	720
CTGGATTTGT TTACCGAGAA GATTTGTCAC AACCACAGGG GGATGG	766

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 901 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1311

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

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CCGCCACGG TTCCATCCAA CTCACAGGT GTGCACTGA TTGTGTATGT AATTGTCACT      60
AACGGTAGAA TTTCACCTAT CCTCCTATC TGCTCGCAGT ACCCGCAGAC TTTCTGAAAG      120
AAGAAGATAA CCTACTTATC CGTTGCTATG ATTATACTAA AGTTTCTACT TTTTGCAAA      180
TAGATTTTTA AATTTTGGC TAATTGCTG AATCAGGGTC GGAAGTTTGA CGACCTTGTC      240
ATTGCCTAGT TTTTCGCGTG CAATTTGAG AATGGCACCT GAGTCTTTTG AAGCAAAGAG      300
GAATTTTCTT TTGTCTGTAA AGACTTCGAA GTGGCGGCTG ATTTTGCCTC CAGTGACATT      360
GGCTCCAATC TGATTGATAT GGCTCCAAGG AATCTGGATA AATTGTTTGA CATGACATC      420
TGGGTAAAAT TCCAAAGCCT GATCTCCGAC AAGGAATTTC CCAACTTTCC CAGCGATAGA      480
GAGGTAGGAA GTGCCTGTCG TACTGAGGAG TACTGTTTTG TTAAGTGATT GGGCCATGCT      540
TAGTCTTCTT TACTTTCTCC AAAAAAGGCA TTGTAGAGGG CTTTAATTGC TGCTTTCTCT      600
TGGTCTTTAT TGACAACAAA CATAATAGAA ACTTCACTAG AACCTTGAGA CATCATCTGG      660
ATGTTGATTT TGTTTTTCTA TAGAGCGCGT GTCGCAGTAG CAGTCACTCC GATATGGCTC      720
TTCATTTTTT CACCAACAAT CATAATGATA GAAAGGTCGT GTTCGATTTC TGCATGATCT      780
ACTTTAGCCT TTTGAACCAA CTGACGCAGG ATTTCTTCTT CCTTGATGGG AGTTAGTTGG      840
CGAGAACGGA GAATGATAGA AAGAwCGTCG ATACCTGTTG GCATATGTTT CCAACCGATG      900
T                                                                    901

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## (2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1765 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

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CCCTGTTACG TGGATAATAG GGTAAGACTG CTCAGGATTT CCTAACAAAT CCACCGCTTG      60
CTGCATTCTGA CCCAAACCTG ATCGAAAATT CAAACCAATC CGACTATGGA GCCATTCTTC      120
TACTTCAAAC ATACACATCT CCTTGACAAA AGTCCAATCA ATTATCGCAT TAAAGTATGG      180
TTACTAATAA AAACAAGGCC AGGATTTTCG TCCCGACCTC ITACCTGGTT AGCTAATAAC      240
TAGCTACTAT GAATGTGAAT ATGGGCTAAA AACATCCACT GGACGTTCCA ACTCTTCCCC      300

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1312

ATTTCTGGGA GTTGGGGTAA AAATGTTTAC TGGACGTTCC AACTCTTCCC CATTCTGGG	360
AGTTGGGCTG ATACAGTCTC CCAGACTGTA TCACTCCTCC ATAAAGCTGT TGAAGACTTC	420
TTCAATCATG TTCCATTCGT CTCTGAGTC TTCTGGGATT GGTGCAATT CGCCTTCTGT	480
TCCATCTTCG TTTTCGATGA ATGAGTAAGC TTGGATTTC AACTGTCCGT CTTCTCTTC	540
TTCTGCGTTA ACTGGTACTA GAAGAACATA GTTTTACCA AATCTTCTT TTCCATCAAT	600
TGTCAAAAGG ATTTCAAACA AGGTTTCATT TCCTTGCTCA TCTACTAGTG TGATTAGTTC	660
ACGTTCTTCG TGGTCGTGGT TATGATCGTG TGACATAGCC TCGCCTTTAT ATTAAAATTT	720
TCTATCTAAA TAATTTTGTA AAATCAGCTG AGCTGCTAAC TTATCAATGA CTTTCTTGCG	780
CTTATTGCGA CTGATATCTG CTTGTTCAT CAACATGCGC TCAGCAGCCA CTGTTGTCAA	840
GCGTTCATCC TGATAGTCTA CTGGTAAACC AAAAACTCT TCTAGCTTTG CTCCGTAGCT	900
TGACTAGCTT CTACGCGCGG TCCACTTGTA TTGTTTATGT TTTTAGGCAA GCCCACTACA	960
AATCGTTCCA CCTGTAAAGT ATCAACCAAT TCCTTAACGC GGTCAAAACC AAATTGGCCT	1020
TGTTCTTCAT TTATCTGGAT GATTCAAGC CCTTGAGCTG TAAAACCAAG CGGATCGCTA	1080
ATCGCCACCC CTACCGTTT TGAACCGACG TCCAATCCCA TAATTCTCAT AGGTTATAGA	1140
TCGACTCCTT GTCCTTTGAG GTAGTAGCGA ACCAATTCCT CAACGATTTC ATCAGCTCA	1200
TACTTACGGA TTTGATTTCG TGCATTATTA TAACGAGGAA CGTAGGCAGG GTCTCCACTC	1260
AATACGTAAC CTACGATTG GTTAATTGGG TTGTAaCCCT TATCGTTCAA CGAAGCATAA	1320
ACATCTGTCA AAGTTTCGCT AATTCTTTT TTATTGGAAT CGTCCAATTT AAAACGTACT	1380
GTTTCTTCAG TAAATCCCAT TCTAACACCC TCTTCTCTTA GAATAGTACC ATTATAGCAT	1440
AATTCCTTAC CTTCTACAAT TCAGGCAGTC TATTTATTTG GATTTTCTAT TGTCTGTGCG	1500
CGCCATTTGC CAATCTATCT GAAATATATT TGCTTGGTTC ATTTTTCAAA AGATTTTCCA	1560
AACCAATATT CTTCAGATGT TCCAACCTGG AAGCCTTCTT GACATCCAGA ACTTGAAAAT	1620
CAAACTAGT CGTTGTTTGA AGTTCCGTTG CGCTCAATAG TTTTGTTC AATTGAAAC	1680
CTGCCAATTT ACGAGCTTCA ATGATAGACT TATCCTTCTC CTCCGCTTCA AGAAGAGCTT	1740
TTTGAGTTTC CTCCACTCCA TGTTC	1765

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1346 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

CTTATCCATT CACTTCTTG TCTGTTATTC TATAAATCTT ACTCCTAAGT ATACCACATT	60
TGCCCCCTAGA TGTGAACGAG AGAAACGCTC TAGACATTGC CAAGAAGGAA AAAAAAGGTT	120
ACAATGTAAC AAAATCAAGG GAGGTCTGGA ATGAAGAAAC AAAGCAAGTA CAAAGAGGTC	180
GTTTCCTATC TGAAAAATGG TATCGAGTCT GGACGATTTC CGACGGGTAG TCGCCTGCCT	240
TCTATCCGTC AACTGAGCCT TGACTTTCAC TGCAGCAAGG ACACCATTCA ACGAGCCCTG	300
CTGGAATTAC GGCACGAACA ATACCTCTAT GCCAAGCCTC AGAGTGGCTA CTATGTATTA	360
GAACAAGGGC AACATCAAGA CCTAGAAATC GAGGTTACCG ACGAACATGC CAGTGCCTAT	420
GACGATTTC GACTCTGTGT CAATGAAACC TTGATTGGCC GAGAAAACTA CCTCTTCAAC	480
TACTATGACA ATCAAGAAGG ATTAGAAGAC CTAAGACAGT CCATTACAA ACTCCTCTTT	540
GAGCAAGCTC TCTACTGCAA GGCTAACCA CTAGTACTGA CTTCTGGAAC CCAACAAGCC	600
TTGTTTATCC TCTCTCAAAT ATCCTTTCCT AGACAAGCCA AGGAAATCTT GGTGGAACAG	660
CCAACCTACC ATCGGATGAA TCGCCTCTTG ATTGCACAGG GGCTGGACTA TCAAACGATT	720
GAACGAGGCA TTGATGGGAT TGACTTGGAG GAGCTGGAAG GCCACTTCAA AACAGGAAAA	780
ATTAAGTTT TCTACACCAT TCCCCGATTT CACTATCCCC TGGGACATTC CTATTCTGAG	840
CAAGACAAAC GATCTATTCT TAACTTAGCT GCCAAGTATG ATGTCTATAT CGTAGAGGAC	900
GATTATCTGG GTGATTGGA CTCCAAGAAG GGCCAAACCT TCCACTATCT TGATACAGAG	960
GAGCGTGTC TTTATATCAA GTCCTTCTCG ACCAGCCTTT TTCCTGCCCT TCGTATTACA	1020
GCACTCATTC TTCCAAATGC TATCAAAGAA GCATTGTGG CCTACAAAAA TATCCTAGAC	1080
TACGACAGCA ACCTCATTAT GCAAAAGGCC CTGTCACTCT ATATTGACAG TCAATTGTTT	1140
GAAAAAATC GTTTGGCTCG CTGACCAAT CATGAATCTT ACCAAAAACA AATCGAGGAA	1200
AGGATAACTA AAACACCTTG TCCCCTTCCT CATTATTCCC TACACGATGG yTTATTGCTA	1260
GACCTGAGAC AGTATCCTAA AATCGCCAGT CTCAAACACA GTCAACTGGG cTTGGACTTC	1320
TTTGAAGAGG CCTATTTAAG CACCTG	1346

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 900 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

CTATATTCAG AATATGCCAA AAATTCGGAA TGGTATAAAT TTGCGGAGGG TTCATTTGAC	60
ATATTTTAGAA AACTCCCCCA AAGAATTAAT TTAAAGAAAG ATTTTTCCTAG AATTTTGGCC	120
CCCTTTATTA TTAATTTGCT TAAATTAATC AATAATTATC TAGAGAATAA AGAATACGAG	180
TGGATTGACA AGAATGGAAA TATTTTTTCC TCTCTAGTAT TTTATTTAGA AGATTTAATC	240
TATCCTTGA TTGTIAAACC TTTGTTTGA GAGATAAATT CATTGCGTGA AAAAGGTTTA	300
CTGAAGGGG AATCGGAGCA GCAACGGTAC AAATATTTTA TAACATTGTT TGACAAGGAA	360
GAGAATATAT TAAATTTTGA TAACAAATAT CCCGTTTTAC TGAGGCAAAT ATCGGAGTCT	420
TGTCTTCGGT TCTATACTTA TTTTATAGAA ATTTTATCAA ATTTAGAAAA TGATTTTAGT	480
GTGCTAGAAG AAGAATTAGG GCTAAGGGG AAATTAAATG ATATAAAATT TGGAAAGGGT	540
GATACACACA GCCAAGGAAA AACTGTTTGG ATACTCTTCT TTGATGACGC GAAAATTGTT	600
TACAAGCCTA AAAATTTAAT AATCAATAAC TCACTAAATA CTATTGCTGA GTATATCCGA	660
AAGGTTGATG AAAAAATTAG GATAAGAATA CCTCGAACTA TTGCTTATTC GGATCACAGC	720
TATGAAGAAT TTATTGATTA TCTACCTCTA GAGCAAAAGA AAAATTTACC TGAATATTAT	780
TATAATTTTG GTGTGCTTTT AGCATTTATA TATTTATTTA ATGGGAGTGA TATACATTTT	840
GAAAATTTAA TTTCTATGG AGATATGCCT GTAATAATAG ACTTTGAAAC AATGTTACGG	900

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 862 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

TTATTTTAGCA GAGGCAGTTT TAAATGTGAA GGATTTGGTC AGTCAAACAG TTTTTTATCA	60
GCAGATTATT GGTTAGAAA TCCTATCTCA AACGGATACA GAGGTCGTTC TGGGACTTGG	120
AGGAAAAGCC TTGGTACACT TGATTCAAGC ACAAGAGGGT GGAGAAGTAA GGAACATTA	180
TGGTCTTTAC CATCTGGCTA TTCTTTTGCC GACACGAAAG GCTTTGGCGG ATGTCTTGAA	240
GCACCTGACG GATTTACAGA TTCCTCTTGT TGGCGGTGCA GATCACGGTT ACAGTGAGGC	300
CCTTTACTTA GAGGACTTGG AGGGAATGG CATTGAACTC TATCGAGATA AGCCAGTTTC	360
CACATGGGAT ATTCGAGAAG ATGGACGTAT TATCGGGGTG ACTGAAGTCC TTGCGGCTCA	420
GGATATCTAT GAGTIGGGGG AAAGAGTAGA GCCTTTTATC CTAGCAGAGG GTACGAGAAT	480

1315

GGGGCATATT CATCTTCTG TCAAGGATAG TCGAAAGTCC AGACAGTTTT ATCAAACGGT 540  
 GTTAGGGCTC GAGGATAAAT TCAGTGTGCC TAGTGCTAGT TGGATCGCAG CTGGGGACTA 600  
 CCATCATCAT TTAGCAGTCA ACGAATGGGG AGGAAAAGGT CTGGATCCGC GTAAACAAGT 660  
 CCTACCAGGT TTAGCCTACT ATGTCATCGA AGTCGCACAT AAAGAAGAAC TGTTAACGAT 720  
 TGCCCAACGA GCACAAGAAG TTGACGCACC AATCAAATGG ATGACATCGA TCCAATGGA 780  
 AATCACAGAC TCAGATGGCA TCGTGACCCG TATTCGTTTA GCTAGATAGA TGGTATGTGA 840  
 TGAAGGTAGA GCATCAATTG TA 862

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 650 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCGTTTACAA GATCGCTAAA ATGCATCTCA TGATCGCGAC CACGAATTCC AAGATAGCAC 60  
 GCGCTACCTC AATCATAGAT AGTTCACTTT TTTCTTGCCC AGCAAATACT TCTAATTCCA 120  
 AAGCGTTTCT CCTCATTTAT ACTACTATCG CCAGAGCGAA CAGACTCTGA CCTCATTTTA 180  
 TCATTTACTC TTTATTTTAC GATAATTTTG CGGAATAGTC AAAGGTTAAG GGGGAGAAAG 240  
 TGGCAGGATT AGACTAATTC CAATATAAAA CTCATTCCTT TTTCTGTTGC TCCATTTTCC 300  
 ACAAATCCAA GCGACTTGAA ACACCTCCTA GAAGCATGAT TGTAGGTGTA GATTTTCTTG 360  
 ACTCTCAATT CTTTCCATCC TTTTACTCGA GCCAATTCAA TCAAAGCACT TAGAATCTTT 420  
 TTTCCAAGTC CTCGATGTTG GTAAGCGGAA TTCCCAATCA CAATGGGGAG ATTATCCTGA 480  
 GATAGTGTA TATCCCCAAT TGGAAACCAT TCTCCCTTCT CTTGACTTC AATCCAAAAA 540  
 AGCTCACCAT GCCGATyCAr ATAGGAATAC ATGGCTTCCA AGGTCGcTtG ACTGTAAGGA 600  
 AGCTTCACCC CATCTACGAG GtAAcCAAGT TCACATCCGT GATACCAAGC 650

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1119 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

1316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GATAGCAATC CGCTTCAGAA ACTTCTCGCT TACCTCTAAC TCCGATCGCT AGTTTGGGAG	60
AAGATACTTC CATTCTCATA CTATCTGTTG GCTTTGCAGG CTGTAAAAAC AACTTTTCTC	120
TTGCTACTTC CTGAAAATCT GAATCTTGCA GTTCTTTGCT TTCAAAATAG TCCTGTACTC	180
GCTCCACATC AAAATTCCCA GCTAAAGACA GAGACATGTT TACAGGTTTG TAAAACTTTG	240
TAAAATTTTC TTGCAAATTA GTTAGATTGA TTTGGGAAAT GGACTCCTCA CTCCAACTA	300
TATCAGTTGC TAAAGGTGTA CCAGGATACA AATTCGCTAA AGTTGAAAAG AATAAACACG	360
AATCTGGATC ATCTTGGTAC ATTTCTCGTT CTTGCTGAAT AATATCCTGC TCTGTCAGAA	420
TGGAAGCTTC AGTAAAGTGT GCTGATGTTA CCAATTCATC AAGTAAATCT AAATTTTCTA	480
AAAAATAATC CGTTGCTGAA AAAAGATAGT TTGTTTTTGT AAAGCTTGTA AAGGCATTAC	540
TATCTGCACC TAGACTCGTA AAAGCCGACA TCAAATCACT AGAATCTTCT CTCTCAAATA	600
ATTTATGTTT AAGAAAATGA GCAATTCCTC CAGGATATTG TTTTACATCT CCGTCAACTT	660
CTGTGACAAA CGTATCTACC GAACCAAACGT GTACAGTGAC ACTCCCGTAA ACCTCTTTAA	720
ATTCCTTTTT AGGCAAAAAG GCAACTGTCA ATCCGTTGGC CAAACGAGTT CGATAAACCA	780
TTTCTTTTAC AGCTGGATAG TATTTTCTT CAAAAACAAC CTTTGTCAAT CTATTCCTTC	840
CATAAAGTAA ATCGCTTGTA GTTTCACATT ATTAGCTACT CTACAAATAG CATCTTTGTC	900
AATTGTGTCA AGCTTTGCAA TCCAACTTTT AAAGTCTGCT GAAGATTTTC CAAATAAGGC	960
ATTTTGATAA GCACGTTCAA TCAATGAAGA ATGATTATCT TGAGAAAGTA ACAACGACCA	1020
ACGAATCATT TCCTTGGTCT GATTTAACTC AAACCTCTGA AAAAAACCTT TTTTAAATC	1080
AAGCCGTTGA TTATTCATCA ATTTACGAGC CTGGTTACG	1119

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 540 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ACGCCCTCGC GGGGACATGA CGAATTCCTC GTTCATCAGC AAGGCCGCCG AGGAGTGGGG	60
GGTGCCGTCC AAGTCAAAAG CGGCCCCACA TCGATTCACT TCCCCGACGA ACAGCCCTTT	120
CCCCAGCGT TCCTGGCTTT GCAACCGTTT CACAACAGCC TCGTAAAGTA GGCCGGACAA	180
GGCAGACGGA CTCCAAAGGA GTTCTTCCAT CTGCAAGTGC GCCTGCGTTA TGTGATCCCC	240

1317

GTCTTTTGCA TGTGTGTGGC ATGAATGCTG TTCCCAATCC CACTCCAGAA CATTCCTCCTC	300
AAAAGTGCGC AACGTCGCCC TGAATGAATC CTGCCTTGTA GTCGTGACCA TTCCTATGAA	360
GGGTCGCAGA GGATTTTCCC CGAGTGCAAG CGCATCCTCC GGCTCAAATC GGGTGCATTT	420
CACAGTCCCG CTCAACGCTA GCCCGATCCC TTTTGGCAT GGTGACTCAA GCGTCCTTTC	480
AAACAAAAGC TCCTCATCCG CTCCAACCGG CCCGACGTAG ACGCGTAGAC CGAAGTCGTC	540

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1949 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AAAGAATTCG ACCAATTCAG GGTGAGGCA TCGCAAACTA TGGACTGTTC CCCCCTCAGT	60
TCTGGACAGA AAACGGGATA AGGTTGGCTG TGAAGCAAGC TGCCCTCCTA CCAACAATTT	120
TGGAAAGTAG GCATCAGCTG ACAATTCTTT ACAAGCATAG TCCGTTCCAT AACCTGTAA	180
CAGTTGAAAG AGGAACTGGA CAAGGATATC TGAATCCGAA TAACGACAGT AGCGGCGTTG	240
GTCATTCGTT ACTAAATACT TAGAAATCCG CTCTTTTAGT TTCAACTGGG AAAAAAGTTC	300
CTGAAAAAAG ATAAGACCAC CATACTGGGT TAAATGACCT CCATCGAAAG ATAGTTGGTA	360
AAAAGACTTG TTTTGGAGT GATGATTTGG TAAACTGTTC ATGTGAGTTT CCTTCTTTT	420
TGTGTTTTTT TCTACACTTA TACCATAAAG GGGAAACTCT TTTTTGTCTA GTAAAAACA	480
CCCATTGGGT GAAAAAAGAA ACCATCCAGG ATCTAAGCTA AGGCAAGGAT TCTGGATGGT	540
TTTTAGATTT GGGGTGAATA ATTGGGGTTT TACAATATCA ACTCCCATGA TAGTCATGAG	600
ATGACTCTTC ACGAATTGAC GTGATGACTG TCCTTCCTTT TGCATAATTA CCTCCGAAAC	660
ACAAAAAAG GGGTAGACAA TCTAGTGTCT ACCCCCGAAA GTTTATTAAA AAAAAATCC	720
TGCCAAAGAA TTTTGGCAG GAAACCAAT CAATTTATCA GTTCTATCA ATCGCTTATC	780
GCTCTCAAAG ACTGGTAAAT AGGATATCCG CAATCAAATT GCGATACTCT ATTATTTAAG	840
AGTAACTGAA GCTCCAGCTT CTTCCAATTT AGCTTTGATT TCTTCAGCTT CTGCAGTTGC	900
AACGCCTTCT TTAACAAGTG CTGGTGACCC GTCAACAAGT TCTTTAGCTT CTTTAAGACC	960
AAGACCAGTG ATTTACGTA CAACTTTGAT AACGCCAACT TTTTGTGCG CTGCAGATGT	1020
CAATTCAACG TCGAATGAAT CTTTAGCAGC ACCAGCATCA GCTGCATCAG CTGCAGCAAC	1080



1318

AGCTACAGGA GCAGCTGCAG TTACACCAA TTCTTCTTCG ATAGCTTTTA CAAGGTCGTT	1140
CAATTCAAGG ATTGAAGCTT CTTTAATTTT AGCAATAATG TTTTCAATGT TCAATGCCAT	1200
TGTTATTTCC TCCAAATAAG TTTTAAATTT TATAATACTT TTTTTCGTAG CTAGkTACG	1260
CTGTGTAGCT TAAGATTAAG CCGCGTCTTC TTTGCTTTCT GCAACCGCTT TGACTGCAAG	1320
AGCAACGTTG CGCACTGGCG CTTGAAGTAC AGAAAGGAGC ATAGAAAGAA GTCCTTCGCG	1380
GTTTGGAAGA GTTGCAAGTG CAAGAATCTC TTCTTTAGAT GCGACAGCGC CTTCGATTGC	1440
ACCACCTTTA ATTTCAAGTG CTTCAGCGTT TTTAGAAAAG TCGTTCAAGA TTTTCGCTGG	1500
TGCGATAACA TCTTCATTAG AAAATGCTAC TGCAGATGGT CCAACAAATA CAGATGCAAG	1560
ATCTTCAAGA CCAGCTTTTT CAGCTGCACG ACGCAAGATT GAGTTTTTAA TAACTTTATA	1620
CTCAACTTCG CTTCCACGAA GCTCACGACG AAGAAGTGTA TCTTGCTCAA CTGTCAAAC	1680
ACGAGCGTCT ACAACGACGA TAGATGCAGC AGCTTTCATT TTTTCAGCTA TACGTCAACT	1740
AGTTCGCTT TTTTAGCAAT AATTGCTTCA CTCATTAGTG TGTTCACCTC CGTAATTATT	1800
TTGCTTGGGG AATTTTTCAA AAAGAAAAC GCGCCCAATC CTAGACACGA AAGTACAATA	1860
CGCTTCTTTT TACATGATAC GTTTTGTCTT CCGTAGGATA TTTATGAGTC GAGCTCCCCT	1920
ACTGTCTTAG GCAGTTTTTT TAGATACGG	1949

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1023 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GGACTGTTTG ATCTTATACA GTAGTGCTT GATCCAAGCT TTCACCGATA GCGGCTAGGC	60
GCTCGATAAC TTCAGCTTGT GTCAATTCAT TTTTGAAC ATAGCGGTTA CGTGGGTGAA	120
CACGGCACTC GTGTGAGCAT CCACGAAGGT ACTTGTCTT ATTTCTTCT GATGTCAAGA	180
TACGACGGTT ACAGAAATGGA TTTCCACAGT TGACATAACG TTCACATGGT GTTCCATCAA	240
ACCAGTCTTT CCCTACGATA GTTGGGTGA CATGGTTGAC ATCAACGGCA ATACGCTCGT	300
CAAAGACGTA CATTTTCCCA TCCCAAAGCT CACCTGAAC TTCTGGGTCT TTACCGTAAG	360
TTGCGATTCC TCCGTGCAAT TGGCCGACAT CTTGTAGCC TTCACGGACC ATCCAGCCTG	420
AGAATTCTC ACAGCGAACG CCACCTGTAC AGTAAACCAC GACACGCTTG TCCATGAATT	480
TTTCCTTGTT ATCACGGACC CATTGTGGTA ACTCACGGA GTTGCGAATA TCTGGCGGAA	540

1319

TAGCTCCACG GAAATGTCCT AGGTCGTACT CATAATCGTT ACGTGTGTCA AGGACAACGG	600
TATCTTTATC AAGAAGCGCT TCTTTGAACT CTTTGGAGA CAAGTAAGCA CCTGTTGTTT	660
CAAGTGGGTT GATGTCATTG TCAAAGTCGT TGTCTTCCAA ACCAAGGTGG ACAATTTCTT	720
TCTTGTAGCG AACAAACATC TTCTTGAAGG CTTGTTTCATT TTCTTCGTCA ATCTTGAACC	780
AGAGTTCTTC CATTCCTGGA AGGCTGTGAA CGTAgTCCAT GTATTTTGA GTTGTTCAT	840
AGTCACCTGA AACTGTTCCG TTAATTCCT CGTCAGCGAC TAGGATACGG CCTTTAAGGn	900
CGATTGATTT ACAGAAAGCC AAGTGGTCTG CAGCAAATG CTCTGCATTT TCAATTGGAG	960
TATAAAGGTA GTAAAGTAAG ACACGAATAT CTTTgkCaw AAGATTGTA TCTCTTATC	1020
TAT	1023

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3831 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

ACTATGAACA AGACCCAGAA AAAGTAGCCT TATTTCTTAA GAATTTAAT AGTTTAAAGC	60
ACCTAGCACC TGTTTAGATT GACGAAACAG GATTCGATAC TTATTTTAT CGAGAATATG	120
GTCGCTCATT AAAAGTCAA TTAATAAGAG GCAAAGTATC TGGAAGAAGA TATCAGAGGA	180
TTTCTTTGGT TGCAGGTCTA ACAAATGGTG AATTAAATCGC TCCAATGACT TACGAAGAGA	240
CGATGACGAG CGACTTTTTT GAAGCTTGGT TTCAGAATT TCTCTTACCA ACATTAACA	300
CACCATCGGT TATTATTATG GATAATGTAA GATTCCATAG AATGGGGAAG CTAGAACTTT	360
TATGCGAAGA GTTTGGGCAT AAACCTTTTAC CTCCTCCTCC CTACTCGCCT GAGTACAATC	420
CTATTGAGAA AACATGGGCT CATATCAAAA AGCACCTCAA AAAGGTATTA CCAAGTTGCA	480
ATACCTTTTA CGAGGCTTTT TTATCCTGCT CTTGTTTCAA TTGACTATAT TAGAGGCGAG	540
ACATTTTTCG GTTCTTTGTC AACTGTAGTG GGTGAAGAA AGCGAAGATC TAGAAAGGAC	600
AAATTCGTC CTTTCTTTT TGAAGTTTTC AAAGTTCCTA AAACCAAAGG CATTGTGCTT	660
GATAAGTTTG ATGAGATTAT TGGTGGCTTC CAGTTGGCG TTGGAATAAC GTAATTGAAG	720
GGCGTTGACG ATTTTCTCTT TATCTTGAG GAAGGTTTA AACAAAGTCT GAAACAGAGG	780
TGGAAGCA AGAGCTGATA GAGATTATAG TGGTGTAA AGTCTTCGGA ATAGCTCAAA	840

1320

AGTTTATCTA GAATTTCTTT ATTAGTCAAG TGCATACGAA AAGTAGGGCG ATAAATCGT	900
TTATCACTCA GTTCTGACT ATCTTGTTGA ATGAGCTTCC AGTAGCGCTT GATAGCCTTG	960
TATTCATGGG ATTTCCGATG ATGGCTTG TGCTGCTCTC AAGAACAGTT ATGATATTGA	1020
GTTTATCAAA GTCCTGAGCA ATAAAGCTCA TCTCCATCTC CCGATTGAAA CAGTCACTCC	1080
CCGGA CTGTT TCAACsTCCT AGGACATAAT CTCAGGAAGA CGCGAAAAAT CATGCTCAAA	1140
GTGAAAATCA TTGTTCTTGC GAATGACAGT TGAAGTTGAA ATAGACAACT GATGATCAAT	1200
GTCGGTCATA GAAGTCTTTT TAATTAGCTT CTGAGCAATC TTTTGGTTGA TGATACAAGG	1260
AATTTGATGA TTCTTCTTGA CGATAGAAGT CTCAGCGAGC TCCATTTT TG AGCAATGATA	1320
GCACTTAAAA CGGCCITTTT TAAGAAGAAT TCTAGTTTGA ATTTTTTTAT ACTAGAAAA	1380
CAGAACCATA ATACCTATAT AAAAATATTA TAGTTCTAAT AGGATTTACC CAAAACITTT	1440
AAGCGGTCT TTTTAGAAGT TTAATTGTTT GAAATTTAGG TAGCAAATTT GTTCTATTT	1500
TGTCAACTTT TCCTATTTTT ATCTTGTTGA GGCTGGTATT TTAACAATTC AGGAATTGAT	1560
AGTGAATGTG TAAAAITTTT TGTTAGAATA AGTTTATAAA AAAGAAAAGG AGTATTTGAT	1620
TATGTTACAA AAAATTTATG AGCAGATGGC TAATTTCTAT GATAGTATTG AAGAAGAGTA	1680
TGGTCTTACA TTTGGTGATA ATTTTGACTG GGAACATGTT CATTTTAAAT TTTAATTTA	1740
TTATTTAGTG AGATATGGCA TTGGTTGTCG TAAGGATTTT ATTGTTTACC ATTATCGTGT	1800
TGCTTATCGT TTGTATCTTG AAAAATGGT AATGAATCGG GGTTTTATTT CTGTGTGAGG	1860
TAATTTTAGT AAATTTCCGA ACTAATTTAC TCTTTTATGG AAAGATGATA GTAAATAGCT	1920
AGTAATTTTT CTAAATCATT TTTAATAGT TGGAAATAGC AAATCTTTCT ATTGTTTCTT	1980
CTTGATAAAA AGGCGATTTT TTAATATAAT AAATTGTAAG ATATAATTGC AGGTGAGAGT	2040
CCTGCCATGT ATGTGAGAAA GCAAGAGCCT GATGGCTCAG ACAAGATTAT GACTTCAGTT	2100
GTGTTGTAG GTACCCAATG GGGTGATGAA GGTAAAGGGA AGATTACAGA CTTCTTTTCA	2160
GCGAATGCAG AAGTGATTGC ACGTTACCAA GGTGGTGATA ATGCTGGTCA CACGATTGTG	2220
ATTGACGGTA AGAAATTTAA GTTGCACTTG ATTCCATCTG GGATTTTCTT CCCTGAAAAA	2280
ATATCTGTCA TTGGGAATGG TATGGTTGTA AATCTAAAT CTCTTGTAAG AGAGTTGAGC	2340
TATCTTCATG AGGAAGGTGT AACAACTGAT AACTTGCGTA TTTCTGATCG TGCGCATGTT	2400
ATTTGCGCTT ATCATATCGA GTTGATCGC TTGCAAGAAG AAGCTAAGGG CGACAATAAG	2460
ATTGTTACGA CAATTAAGGG AATTGGTCCA GCTTATATGG ACAAGGCTGC TCGTGTGGA	2520
ATTCGTATTG CAGATCTTTT AGATAAGAT ATTTCCGTG AGCGTTTGA ACCTAACCTT	2580
GCTGAAAAGA ATCGTCTTTT TGAAAAATTG TATGACAGTA AAGCGATTGT TTTGATGAT	2640

1321

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ATTTTGAAG AATATTACGA ATATGGTCAA CAAATCAAGA AATACGTGAT AGATACATCT 2700
GTTATCTTGA ATGATGCGCT TGATAATGGC AAACGTGTGC TTTTGAAGG TGCACAAGGT 2760
GTTATGCTAG ATATCGACCA AGGTAATTAT CCATTGTGTA CGTCATCAA CCCTGTAGCT 2820
GGTGGTGTGA CAATTGGTTC TGGTGTGCGT CCAAGCAAGA TTGACAAGGT TGTAGGTGTA 2880
TCTAAAGCTT ATACGAGTCG TGTAGGAGAT GGTCTTTTCC CAACTGAGTT GTTTGATGAA 2940
GTGGGAGAAC GTATCCGTGA AGTGGGTCAT GAATATGGTA CAACAACGG TCGTCCACGT 3000
CGTGTAGGTT GGTTCGACTC AGTTGTGATG CGTCATAGCC GTCGTGTTTC TGGTATTACT 3060
AACCTTCTCT TGAAGTCTAT TGATGTTTIG AGCGGTTTGG ATACTGTGAA AATCTGTGTG 3120
GCCTATGATC TTGACGGTCA ACGTATTGAC TACTATCCAG CTAGTCTTGA ACAATTGAAA 3180
CGTTGCAAGC CTATCTATGA AGAGTTGCCA GGTGGTTCAG AAGATATTAC CGGAGTTCGC 3240
AATTTGAAG ATCTTCCTGA GAATGCGCGT AACTATGTTT GTCGTGTGAG TGAATTGGTT 3300
GGCGTTCGTA TTTCTACTTT CTCAGTAGGT CCTGGTCGTG AACAAACAAA TATTTTAGAA 3360
AGTGTTTGGT CCTAAGAGAT TTTTAAGATT TGTTTAAGAT AGGTCGGGTA TACTATAGAC 3420
GTTTACAAGA AGACCTCCTA ACTTGTGTTA ACAAATATCC TAAACTTTTC TTTTTCATAA 3480
TAATCTCCCT ATAGAGTCAC CGCATTCGGT GGCTTTTTTT GTGTTGGGAT TCATGATATA 3540
ATAATAAAAT CGATAAGTAG GAAAAGAGAA AAGAGATGTA TTATACGCTT GAAGAAAAAG 3600
AAGTCTTTAT GAGGGAGGCT TTGAGAGAGC CTGAGATTGC TCTTGAACAC GATGAAATTC 3660
CAATTGGTTG TGTGATTGTC AAAGATGGGG AAATCATTGG TCGTGGGCAT AATGCGCGTG 3720
AGGAATTACA GCGAGCGGTT ATGCATGCGG AAATTATGGC TATAGAGGAT GCGAACTTGA 3780
GTGAGGAGAG TGCCTTGCT GGATGCACA CTTTTGTGA CCATTGAACC G 3831

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(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1441 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

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CCGCTGTTC AACCGCAACA TACCATAGTC CGTACGGGAT TCGAACCCGT GTTACCGCCC 60
TGAAAAGGCG GATGACTTAA CCCCTTGACC AACCGACCTG AGTTGTTATT TTCAACTCTT 120
ACTATTATAC AGTCTTTTCA AACTTTGTCA ACTACTTTT CTAATTTTGTG TTTATTTT 180

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1322

CAACTTATAG TAAAAAAGC CAGAATTATA CTGACTCTTC TATCGCTCAT TAAACTTAGA	240
AGCACGTTCT TTTCCCCACC AATAAGGGAT TAGTTCTGCG ACTTTAACTG TTTTCTTAT	300
ATTATAGTCC ATCATGAATT CTGCATCTTT ATTTTCAGCA TTAAGCTCTA AAAGGAATTC	360
TCTACAAGCA CCGCAAGGCA TGGCTGAACT TCCACCATAA GGTGGTTTGT CTCGAAAGGC	420
TAATACTTTC TTAACCTTAG TTTGTCCTGA AAATTGGTAC ATATTGAAGA GGGCCGCCCG	480
TTCTGCGCAG AGATGGAAAA CACCACAGGT TCCCTCCATA CAGAATCCTG TAAATATTTG	540
TCCATCTCCT GCTTCTACTG CAGCTACAAC ATGATTGGCA TAAACAAAGT CTGATACTTC	600
ATGTGGATTG TATAGTTTCT GTGCTTCTTC GTACATCTTT TCCCAGATGT CCATTATTGT	660
ATCCTCTTTA TTTAGAGATT TCTTTTAGCA TGTTTTCGAT ATGCTGAATT GATTTTTCAC	720
GTCCAAGCAA GAAAATGTA TCTGGTAATT CTGGCCCATG CATTTGCGCT GAAACTGCCA	780
TACGAATAGG CATGAAAAGA TTTTCCCTT TAATACCTGT TTCTTTTGG ACTGCTTTAA	840
TTTGTGGGAA GATATTTTCT GTCACAAATT CATCATCTGT CATCGCTTCA AGTTTGTCTT	900
TGAATGCTTC AAGAACTGTT GGAAGTGTTC CACCGTCAT GACTTCGCGC TCTGCTTCTG	960
TCAATTCTGG GAAATCTGAG AAGAAAAGAT CTGTCAATGG GATAATCTCA TCTACTGATT	1020
TCATTTGTGG TTTATAGAGC TCAACTAATT TTTCAGCCTT GTCAGTCAAA CGGCCTGCTT	1080
CCTCTAAGAA TGGTTTGGC ATTTCAAAGA TGGTTTCAAG GTCTGCATTC TTGATATAAT	1140
CATTGCTCAT CCAGTCTAGT TTTTCTGAT CAAAGGCTGC TGGTGACTTG CTGAGGCGGT	1200
TTTCATCAAA AAGTTTAATG AATCTTCAC GAGAGAAAAT CTCATCCCCA CCACCTGGGT	1260
TCCAACCAAG AAGAGCAATA AAGTTAAAGA CTGCTTCTGG AAGGTAACCT TTCTTTCGGT	1320
AATCTTCGAT AAATTGAAGT GTATTAGTAT CACGTTTAGA TAACTTCTTA CCAGTTTCAG	1380
AGTTGATAAT CAAGTGTCAT GTGACCGAAC TCTGGAGCTT CCTCAACCTA AGAGCGGGTA	1440
T	1441

## (2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4398 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

CGGCTTATGT AGTGGCAATC TTTCTACGTA AGCGAAACGA GGGGAGATTA GAGGCGCTAG	60
AAGAAAAAAA AGAAGAACTA TACAATCTTC CAGTAAATGA TGAAGTAGAA GCTGTAAAAA	120

1323

ATATGCACTT GATTGGACAA AGTCAAGTGG CTTTCCGTGA ATGGAATCAA AAATGGGTCG	180
ATTTATCTCT CAACTCTTTT GCCGATATTG AAAATAATCT CTTTGAAGCA GAAGGCTATA	240
ACCATTCATT TCGTTTCTC AAGGCCAGTC ATCAAATGA CCAAATTGAG AGTCAAATTA	300
CTTTGATTGA AGAAGATATT GCGGCAATTC GCAATGCTTT GGCAGACTTA GAGAAGCAAG	360
AATCTAAAA TAGTGGTCGT GTTCTTCATG CTTTGGATTT ATTTGAGGAA CTTCAGCATA	420
GAGTTGCTGA AAATTCAGAA CAGTATGGTC AAGCCTTGA TGAAATTGAA AAACAATTAG	480
AAAAATATCCA ATCTGAATTT TCACAATTTG TAACCTTGAA TTCATCGGGT GACCCGTGTG	540
AAGCCGCAGT GATTTTGGAT AATACAGAAA ATCACATTTT GGCCTTAACT CATATGTGTG	600
ATCGTGTTCC AGCCTTGGTT ACGACGCTTT CTACAGAATT GCCAGATCAA TTACAGGATT	660
TGGAAGCCGG TTATCGTAAA CTAATTGATG CTAATTATCA TTTTGTGTA ACGGATATTG	720
AAGCGCGTTT CCACCTTGCTT TATGAAGCAT TCAAGAAAA CCAAGAGAAT ATTCGTCAGT	780
TGGAATTGGA TAATGCCGAA TATGAGAATG GACAGGCACA AGAGGAAATC AATGCCTTGT	840
ATGATATTTT TACTCGAGAA ATTGCTGCTC AGAAAGTAGT GGAAAATCTA CTGCAACTC	900
TTCCAACCTA TCTTCAACAT ATGAAAGAGA ATAATACTTT ATTTGGGAGAA GATATTGCAC	960
GTTTGAACAA GACCTATTTA CTTCTGAGA CAGCTGCAAG CCATGTTCGT CGTATTCAGA	1020
CAGAATTAGA GAGTTTGTAG GCAGCTATTG TTGAGGTAAC TTCAAATCAA GAAGAACCAA	1080
CCCAAGCTTA TTCAGTTCTT GAAGAAAATC TTGAGGATTT ACAAACCTCA CTAAAAGATA	1140
TTGAAGATGA GCAAATTCA GTTAGTGAGC GCCTGACACA AATTGAGAAA GATGATATTA	1200
ATGCACGTCA AAAGCCAAT GTTTATGTCA ATCGTCTCCA TACTATCAAG CGATACATGG	1260
AAAAACGCAA TCTGCCAGGT ATTCCACAAA CTTTCTTGAA GTTATTCTTT ACGGCAAGCA	1320
ATAATACCGA GGATTTAATG GTTGAGTTAG AACAAAAAT GATTAACATT GAATCTGTTA	1380
CCCGAGTTCT TGAAATTGCA ACGAATGATA TGAAGCTTT AGAAACGGAA ACTTATAATA	1440
TTGTACAATA TGCAACTTTG ACAGAGCAAC TCTTGCAATA TTCTAACC GC TATCGCTCAT	1500
TTGATGAACG CATTCAAGAA GCATTTAACG AAGCTTAGA TATTTTGTGA AAAGAATTGT	1560
ATTATCACGC TTCATTTGAC AAGATTTCTC AAGCATTGA AGTGGCAGAG CCTGGTGTA	1620
CCAATCGCTT TGTACCTCA TATGAGAAAA CACGTGAAAC GATTCGTTTT TAATAAAAGA	1680
AAAAGATTTT ATTTGTGTAG GAGCAGAATC AAATCTTTTT CTATAGTTGT GGGGAGATTT	1740
ACTTCATTTT CTCCTGAGAT TGAGTTTTTG CCCAGCCGAT TTATCCACTA CCTCAAAACA	1800
GTGTTTTATA CTCTTCGAAA ATCTTTTCAA ATCACGTCAG CGTCGCCCTA CCGTACTCAA	1860

1324

GTACAGCCTG AGGCTAGCTT CTTAGTTTGC TTTTGTGATTT TCATTTAGTA TTAAAGTGAT	1920
TTCCGCCAGTC TTATCTGCAG CTTCAAATCT GTACTTTGAG TAACTTGGTA ACCGTCCAAT	1980
AACGAAGTCT ATTGAAAAAT CTCAGACTA GAGAACTCAC GGATAGTTCC TAATCTGGAG	2040
ATTTCTTATT TGCACCTTTC TTGTACAAC TTAGTCCACG GTAAATAGAC CTCTAAAACC	2100
TCTTTGTTTA CGAGAGTTTC CTCGTTTGA ACACATTCTA GAAGATAGGA TAGATATTTT	2160
TCGTATTTA TACTAGACTA AAATCAAAAA GCATTATATA ATAGTGATAT GAAATCAACT	2220
AAAGAAGAAA TCCAAACCAT CAAAACACTT TTAAAAGACT CTCGTACAGC TAAATATCAT	2280
AAACGCCTTC AAATCGTTCT ATAGTAAAAT GAAATAAGAA CAGTACAAAT CGATCAGGAC	2340
AGTCAAATTG ATTTCTAACA ATGTTTGTAGA AGTAGAGGTG TACTATTCTA GTTTCATCT	2400
ATTATATTTT CTCTGATGGG CAAATCTTAT AAAGAGATTA TAGAACTTTT ATAGTAGATT	2460
GAAATAAGAT GTGAACAACT CTATCAGGAA AGTCAAATTA ATTTATAGAA ATATTTTAGC	2520
AGCCAAGGTG TACTGTTATA GATTCAATAC ACTATAGACT GTAATCAAAC AACGATTTGG	2580
CGAAATGTAA AAAAATATGA GGAGTTCGGA CTCGACTCTC TCCTTCAAGA AACACGTGGT	2640
GGTCGTAAAC ATGCATATAT GACAGTTGAG GAAAAGAAAG TCTTCTTGC CCGCCATTTG	2700
AAGGCTGCAG AGGCAGGAGA ATTTGTTACA ATTGATGCCT TATTTCAGGC TTATAAAAAG	2760
GAGTTAGGTC GTTCCTACAC ACGTGATGCC TTCTATCAAC TGTGAAGTG CCATGGTTGG	2820
CGAAATATTA TGCCACGTCC AGAACATCCT AAGAAAGCAG ACGCTCAAAC CATTTGTCGG	2880
TCTAAAAATA AAATCTCAAT TCAAGAAGAA AAGAAAGCGC TTTAAAACCA GTAGACGTTT	2940
TCGTAAGGTT CGCTTGATGT ACCAAGATGA GGCTGGTTTC GGTAGAATCA GTAAACTGGG	3000
ATCTTGTTGG GCTCCAATAG GAGTAGGTCC ACATATCCAT AGTCACTATA TACGAGAATT	3060
TCGCTATTGT TATGGAGCTG TTGATGCCCA TACAGGCGAA TCATTTTCT TAATAGCTGG	3120
TAGATGTAAT ACTGAGTGGA TGAACGCCCT TTTAGAAGAG CTTTCACAAG CTTATCCAGA	3180
TGATTATCTT TTACTCGTTA TGGACAATGC TATATGGCAT AAATCAAGTA CCTTAAAGAT	3240
TCCGACTAAT ATTTGGTTTA CCTTTATTCC TCCATACACA CCAGAGATGA ACCCCATTGA	3300
ACAAGTGTGG AAAGAGATTC GTAAACGTGG ATTTAAGAAT AAAGCCTTTC AAACTTTGGG	3360
AGATGTCATG AATCAACTCC AAGATGTTAT ACAAGGATTG GAGAAGGAGG TGATAAAGTC	3420
CATCGTTAAT CGGAGATGGA CTAGATGCT TTTTGAAAAC AGATGAGTAT AAAAAGAAAG	3480
TCCTCATTTT AATAGAAATC ACGACTTTCT GATGGATTTA TAGTAAATG AAATAAGAAC	3540
AGGACAAATC GATCAGGACA GTCAAATCGA TTTCTAACAA TGTTTTAGAA GCAGAGGTGT	3600
ACTATTCTAG TTTCAATCTA CTATATTTT GGAGTGATAG AAAAGCCCTT CATAAGCTAG	3660

1325

TCTACTTGTT CAGGTGCGAG AGCTTTGACA TCTTTTCTG TACTTAGCCA AGTCAGTTTT 3720  
 CCGTTCTCAA AGCGTTTATA TAGTAGCCAA AATCCTTGAC CATCCCAGTA AAGGGCTTTA 3780  
 AAGCGGTCTT TACGTCCACC ACAAAGAGA AAGACTTGAC CGGAGAAAGA ATCCAATTCA 3840  
 AAGTGGGTTT TAACTACATA GGCTAATGAG TCTATTCCT GCCTCATATC TGTCTTGCCA 3900  
 CAAACAAGGT GAACCTGACC TAAATCACTT AGTTGAATTA TCATAGTACA ATACCTTTCC 3960  
 TCCGATAATT ATTTTATC TAGTATACTG GAAGTTGGGG AATTAGGATA GATACCTTGT 4020  
 TATGACGCGC TTACGTAAC TGTAACTAGC TGCCTAGTTT GATCTTTGCT TCTTCATTGA 4080  
 TTAGCAGTAG ATTTCAAAAT GATAAAAACG CATAGTATCA GGTATTGAAA TGTACTGCCC 4140  
 CAAAAGTTAG ACAGAAAAA TCTAACTTTT GGGGTGTTTT TGTATTGAAA TTAAGTTATG 4200  
 ATGATAAAGT TCAGATCTAT GAACCTAGAA AACAAGGATA TAGCTTAGAG AAGCTTTCAA 4260  
 ATAAATTGG GATAAATAAT TCTAATCTTA GGTATATGAT TAAATTGATT GATCGTTACG 4320  
 GAATAGAGTT CGTCAAAAA GGAAAAATC GTTACTATTT TCCTGATTTA AAACAAGAAA 4380  
 TGATTAATAA AGTCTTAC 4398

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 718 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AGATTTTGTAG ACTTTGTCTT TAATCGTTTC TTTTAGGGA TGATTGCGAC ACCTTCTTTT 60  
 GGCTATTAAAC TTTAGCAGGA GGGATTATCC TTGGTCTAGC GCCGGCTAGT GCCACCTTGA 120  
 TGAGCTTATA TGCAGAACAT GGTATAGCT TTCGGGAATA CAGTTTGAAG GAGGCTTGGT 180  
 CTCCTTACAA GCAAAATTTT GTCTCAAGCA ACCTGATTTT CTATAGCTTT TTAGGTGTGG 240  
 GTCTAGTTTT GACCTATGGT TTGTATCTCT TGGTGCAATT GCCTCATCAG ACCATTGTTC 300  
 ATTTGATTGC GACCCTTTGG AATGTCCTAG TAGTTGCCCT GATCTTTTGG GCTTATACAG 360  
 TATCTTTAAA ATTACAAGTT TATTTTGCCT TGTCTATCG AAATAGTCTC AAATTATCCT 420  
 TGATTGGCAT CTTTATGAGT CTAGCAGCTG TGGCTAAGGT TCTCCTTGGG ACTGTGCTAC 480  
 TTGTAGCAAT TGGTTATTAT ATGCCTGCCC TGCTATTTTT TGTAGGAATT GGGATGTGGC 540  
 ATTTCTTTAT CAGTGATATG TTGGAACCTG TCTATGAAAT CATCCATGAA AAATTGGCGT 600



1326

CAAAATAGAA TGAAGCAGTT TTGGCTACAT ACGCTTCTAA GAACCTATAG TTCAGTGATG	660
ATCATTATCA TTGCGAGTTT TGCAATCTTA CTCTCTTACG CTGTCTGGGA TTCACGTG	718

## (2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 718 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

TCGGTACCAA AATTCTGGAT TTATACTAGC AAAGATCCAA GAGCAAA'TTA TTTAACAGAT	60
TTAGGTCTAG TTTTCCCTGA ATCATTAAAA GAATTTGACA GTGAAGATAG TTTTGCAAAG	120
GAAATTTCTG CAGAAGAAGC AAATAAGATA AATGATGCTG ATGTAATCAT AACTTATGGT	180
GATGATAAAA CTCTTGAAGC TTTACAAAAA GATCCTCTTT TAGGTAAAT AAATGCAATT	240
AAAAATGGTG CCGTTGCTGT AATTCAGAT AATACACCGT TAGCAGCCTC ATGCACTCCA	300
ACACCACTTT CAATAAACTA TACTATTGAA GAATACCTAA ATCTTTTAGG AAATGCATGC	360
AAAAATGCGA AATAAAAAAC AAATAAACCT AGGCATAATT TTTATAATCT GCCTAGGTCT	420
TCTTATTACA ATATTTTGT CATTAAGCT TGGAACAAAA GAAATTAATA TCAGAGATTT	480
TTTAGCAGCT TTTGGAATGG GTAATACAAA TGATGATTTT ATTAAATCAA TTATATATAA	540
rAGAATACCT AGAACTATTT TTGCAATTTT AGCAGGTCTT AGTCTTGCCA TAAGCGGTGT	600
ATTGATGCAA TCAGTTACTA GAAACCCAAT AGCTGATCCA GGTATACTCG GTATAAACAC	660
AGGAGCAAGT CTTAGTGTAG TAATTGGTCC TTCTTTTAG GGAATTCATC AAGCATAA	718

## (2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GAAC TAATCA TTTTACAGG ATGAGATTTA CAGCAGAGAG TTTGAAGGCT TTATCAAAGG	60
TTTTTCTTGG CATAATGACT TTTCCTCGTT TCCACTTAAT TTTGTGTCTA CTTTATTATA	120
CCAAGTCCAC sCTTAAGTTA GATAATAAAT CTAACCTAAG GAAGCTAGAA GGATGAGAAT	180
CCAGGTGGTC AAGAGTCCCA AACTTAAGCT GATGGGGACA CCCAGAATAA TTTGCTTTTT	240

1327

GAAGGCAAGG CCACGTTTCCT CTATATTGGG AAGTGAGACT TGAATGAGAG AACCAGCTGA	300
TGAAAAGGGT GAGATATTAG TAGATAGAGC GCCAATAACG GTGGCTGTTG TGAGTAAGTG	360
AATATCAATC TCAGGATTTT GAGCACTGAT GATAGCAATG ATGGGAAAGA GGGCTGGAGC	420
TACAACGGAT AGGGTGGAAC TAAAGAGTGA CATCACTCCG GCTATCACAC AAAAGAACAG	480
AGGTAACCAG AAATGAGGAA TGCTTGTTGT CATGAGGTGC CCTATCAGTG TGAATAAACC	540
TGACTTGACC GCTAGAGACA TTAGTAAGCT CATGCCGAG AGCATGATAA TTGTAGCCCA	600
GGGAACCTTA GCTAAAATGG CTTCTTGCTT CCCTAATTTG AGCCTTAAGG CGAGGCAGAC	660
CATGAGTATT GAGACAAAGC CAATATCAAA TGTTTTTTGA TAAGTAGCTA TCCAGGCGAT	720
GTTTGGGAAA ATGAGATGCA ACAAGGGAAA AAGCCAAACC AAAACCATGC TGCTGATCAT	780
GAGCAAGGTG GTTGTCTTT GAACCTTGCT GAGGAGTGGT GGTGGTCAA TAGTCAAGGA	840
TGAGTTTGTT CTTCCCTTAC TATAGTGAAT GTAACAGGAT AATAAAAGCA AGACGATGAG	900
TGGGTAGATA ATGCTGACGA TAAAGATATG ATTGCCAAAGT GAAAAAGCTT GCTCTTCCCA	960
TCCCATTGCG TTAACAGGC CTTGAAAGAC AATGCCTGAG CTACTGGTTA TCAAATTAGC	1020
CCCTCCTGAA GCTCCCAAT TGACGGCTTG AGCTCCAATC AAAGGGTGTT TGTCCGCTTT	1080
TTGACAGAGG GTAATCGCTA GAGGACAGCA AACGGCCATA GTAGTGAAAA ATCCAGCACC	1140
TAAAGCAGAC AAAAGGGTTG CCATCAGGTA TAAATCATG TAGAGGGCGT TAGGGTGGGT	1200
GCGTGTGCGG TAGAGAATGT GTTGAGCCAA AACATCAAGA GTACCGTTAG TTGTTGCAAC	1260
GTTATAAAG AGAGAGACGC TAAAAATGGT AAAAAAGAGT GAGGTTGGCC AAAAATGAAG	1320
AAGTTCTTTG GGGCTTAATC CCATGAGAGT GGTGCGATG AGGTAAGAAA AAGCAATAGC	1380
CAGCAGGCCA ATATTGATTT TGGTGCGGTA ACCAATTCCA ATGGCTAGAG CAATGG	1436

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1696 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

CCATTTGGA AAGAACGTAA GAGTTTGAG GGTGAGATTC CAGAAGAATT TTCAATGTCA	60
GCCGTGACA TGTCTATGAT TGACCACATT CCAGATATGA TTGAAAATGG TGTGGACAGT	120
CTAAAAATCG AAGGACGTAT GAAGTCTATT CACTACGTAT CAACAGTAAC CAACTGCTAC	180

1328

AAGCGGCTG TGGATGCCTA TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC	240
TTGGTGGACG AGATGTGGAA GGTGCCCCAA CGTGAAGTGG CTACAGGATT TTAATATGGT	300
ACACCATCTG AAAATGAGCA GTTGTGTTGGT GCTCGCCGTA AAATTCCTGA GTACAAGTTT	360
GTCGCTGAAG TGGTTTCTTA TGATGATGCG GCACAAACAG CAACAATTCTG TCAACGAAAT	420
GTCATTAACG AAGGGGACCA AGTTGAGTTT TATGCTCCAG GTTTCCTGCA TTTTGAAACC	480
TATATTGAAG ATTTGCATGA TGCCAAAGGC AATAAAATCG ACCGCGCTCC AAATCCAATG	540
GAACATTTGA CTATTAAGGT GCCTCAACCC GTTCAATCAG GAGATATGGT TCGTGCATTA	600
AAAGAAGGAC TCATCAATCT TTATAAGGAA GATGGAACCA GCGTCACAGT TCGAGCTTAA	660
GAAAGGAAAA GGAAATGATA GAGGCACAGG GTTCTTAGT GGATAAGCAA ACAAGATGCA	720
TTCATTACCA TAGCAAGCTG GATATTATTG CTTTACAATG CTATGATTGT AAAAAGTATT	780
ATGCTTGTTA TCGGTGTCAT GATTCAATAG AACATCACCC TTTTGAGCCG TATCCCCTTAT	840
CTTTGATACA GGATAAGCCT ATTTTATGTG GTGTTTGTCT AAAACTACTA ACATATAAGC	900
AATATAAAGA AAGCTTAAGT TGCCCCTTTT GTTTTCTCG CTTTAATCCA GGTTGCCAAA	960
ATCATAAGGA ACGCTATTTT AAATAGCAA TCATCTAGTT TTGAAGTAGG AGAAAACCTCA	1020
ATTTCAAGAG AAAATGAAGT AAATCTTCCC ACAATAAAC GCATAAATATC AAGATTGTTC	1080
AATACCTGAT ACTATGCGTT TTTAAGATTT TAAAGACTTT TTTCTTTAT CTGGTATTTT	1140
GACTACTTGT TAAACTGGG TTAATTTTCG ACTGTTTAAAT AGTTATTATG CAAAGTCTAA	1200
AAGGTTAGAA TTGTCAAAC AATCCGTCTA GAGTATGCGT GATGCCAACC GTGGTGGATG	1260
TTCTCAGTCA TGCCGTTGGA AGTACGACCT TTACGATATG CCATTGTTGGA AAGAACGTAA	1320
GAGTTTGCAG GGTGAGATTC CAGAAGAATT TTCAATGTCA GCCGTTGATA TGTCTATGAT	1380
TGACCATATC TCAGATATGA TTGAAAATGG TGTGGACAGT CTAAAAATCG AAGGACGTAT	1440
GGAGTCTATT CACTATGTAT CAACAGTAAC CAACTGCTAC AAGCGGCTG TGGATGCCTA	1500
TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC TTGGTGGACG AGATGTGGAA	1560
GGTTGCCCAA CGTGAAGTGG CTACAGGATT TTAATATGGT ACACCATCTG AAAATGAGCA	1620
GTGTTTGGT GCTCGTCGTA AAATCCCTGA GTACAAGTTT GTCGCTGAAG TGGTTTCTTA	1680
TGATGATGCG GCGGTA	1696

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1022 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1329

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

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CCGAGTTTAT TATGGTTTCT TCGGAATTTA TCTCAAAGAT TGAATTGCT TGCAATAAGA      60
AAGAAAGTCT TTATAGTCAA AGCAAATTTA AGTATGCGAT TCGTTCGATG TTCGCAGGTG      120
CATTTTTAAC CTTCACTACT GCTGCAGGTG CAGTTGGGGC TGACTTGATT AATAAAATG      180
CACCAGGTAG TGGACGCTTC CTCTTTCCAT TCGTTTTTGC TTGGGGCTTG GCCTACATTG      240
TTTTTTTGAA TGCCGAGTTG GTCACCTCAA ACATGATGTT CTTGACTGCT GGTAGTTTCT      300
TAAAAAAAT CTCTTGAGAGA AAAACAGCTG AGATTTTACT ATACTGTACC TTGTTCAACC      360
TTATCGGAGC CTTGATAGCA GGGTGGGGCT TTGCTCATTC GGCAGCCTAT GCGAATCTGA      420
CACACGATAG TTTCATCTCA GGTGTTGTTG AGATGAAGTT AGGCCGCTCA AATGAATTGG      480
TCTTGCTTGA GCGGATTTTG GCAAATATTT TTGTAAATAT TCGGATTC TG      540
TGGTCAAAGA TGGTGGTGCC AAACCTTGGC TTGTGTTGTC AGCTATTTAC ATGTTTGTAT      600
TCTTAACAAA CGAGCACATT GCGGCGAACT TTGCTTCTTT CGCGATTGTG AAATTCAGTG      660
TTGCTGCGGA TTCAATTGCC AACTTCGGTG TTGGAAATAT GCTTCGCCAC TGGGGTGTGA      720
CTTTCATCGG AAACCTTATC GGAGGAGGCC TCTTGATGGG TCTTCCATAT GCCTTCCTCA      780
ATAAAAACGA AGATACTTAT GTAGATTAAG AAAATGAGCA CGATTGAGTC GTGCTTTT      840
CATTTTCAAA ATAAGGTAAT AGCTATTTCT TATATCAAAA TATAGAAAAC TGATATTGT      900
AACTATAAC TCAAGGTGCT ACAATATCCT TAATAAAATA ATATGGAGGT CACCTTATGA      960
CTTGTTGATTT TAAATnTGAA ACTCTACAAC TACATGCTGG TCAAGTTGTG GCTCCAGCTA      1020
CT                                                                 1022

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## (2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 663 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

CCTTAAGTAA TCTCTGATAA TATTTTCTTT ATTAGCATAG GGAATATCG ATATAATGGC      60
TTCATTATGA GTGGCAGGAA TATCCAATAT GGCAACTTTT CCAATAGATA ATTTAAACT      120
CATTAATAAA GTTCCTTTAG GTGAAATGTC TATTTCCTTT GATTTTAATG CTAATTAGA      180

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1330

AATAGATTCT CTCGATTAG TTACATAACC AGATATAGGC ATATCTGATA TAGATACCCA	240
AGGTATTTC A GTTCCCCAAA AAGTAGCTTC ACTGCGTGGA GGAGTTTTC CTATTCTGAA	300
GTTAACTAGG CTAGCAAATT TAATATATCT CCATGCTTCT GGGATTTCAT ATATAGGATA	360
AGAGGTTGTT TCGTCTTTGT TCCCATATA AGAGTTATCA TCTCCTTGGG AAACAATAGA	420
AATGTCCAAA TCTTCTTTT TAATCTTGCC TTCTTCAAAG AGTTTTGT TTTCTGCTCG	480
TATTTTTTCA AGTAAACTT CGACTGATTC ATCATTGGG TCTTGTTCAA CTAATTTTCC	540
TTGCATAGCA TATTGAAGAA TAGATTTTT TAGTTTATCT GGAAATTCTT TATCTAGCTG	600
TTCTAGTCTA TTATAACTTT CAGCATATTC ATCTACTTTT TCTAAAGCTG ATTCGATTGC	660
TTC	663

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 881 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

CGTCGCTGAA CATGTCAACA GCAAATTA AAACTAAAC TAAAATTATG TGATACTTCA	60
CATAATTTTC TTTAGAAAAT ATTATCAGAA GAAAGTTGAG AAAAATGGCA GAAAAACAT	120
ATCCTATGAC CCTTGAGGAA AAGGAAAAAC TTGAAAAAGA ATTAGAAGAA TTGAAATTGG	180
TTCGTCGACC AGAAGTGGA GAACGCATTA AGATTGCCCG TTCATACGGT GACCTTTCAG	240
AAAACAGTGA GTACGAAGCA GCTAAGGATG AACAAGCCTT TGTGGAAGGA CAAATCTCTA	300
GCTTAGAAAC AAAAATCCGC TATGCTGAAA TCGTCAATAG CGACGCAGTT GCCCAGGACG	360
AAGTAGCGAT TGGTAAAAA GTCACCATCC AAGAAATTGG TGAGGACGAA GAAGAAGTTT	420
ATATTATCGT AGGTTTCACT GGTGCAGATG CCTTTGTAGG TAAGGTTTCA AATGAAAGCC	480
CAATTGGGCA GGCCTTGATT GGCAAGAAAA CAGGTGATAC AGCAACCATT GAAACGCCTG	540
TTGGTAGCTA TGATGTAAAA ATCTTGAAGG TTGAAAAAAC AGCCTAAAA CAGAAAAAGG	600
AGTGGGGAGG CGATGTGCTT CACTCACTCC TTTTTCATT TTGCTACTCT TCGAAAACT	660
CTTCAAACCA CGTCAGCGTC GCCTTGCCGT ATGTATGGTT ACTGACTTTG TCAGTTTCAT	720
CTACAACCTC AAAACAGTGT TTTGAGCTAA CTTGCTCAGT TTCATCTACA ACCTCAAAAC	780
TATGTTTTGA GCTGACTTCG TCAGTTTCAT CTACAACCTC AAAACCATGT TTTGAGCCGA	840
CTTCGTCAGT TTCATCTACA ACCTCAAAAC TATGTTTTGA G	881

1331

## (2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 949 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

```
CCTTTTAA TACAAGTTAT TTTGATTAA CCGGCTTGTG TTGAGCTGTC TGCAAAGCTG      60
TGGCAATCGT ATCTGCATAC AATTTTGCTC CTGCTTCGAT AGTGCTACTC TCACTCCCGA      120
AATGAACCTG GTCTGTTCCA GCCCAAATTT CTGGATGCTC TTTCGCAACT TGATTCCAAT      180
CTGCTATCGT AATGTAAGGT GTCTTCTCTG CCAATTCTCT CATATAGGCA GCAGCCTTCT      240
CAACGATGGC ATAGGTCTCT TTTGTCTTAT CTCCCTCATA AGGAGTCACC AAAATCATAT      300
GGTGTCCCTT AGGAAGATTT TTCACGATAC TGTCCAGTC ATCCTTGTA TTCTCAGGAT      360
TATTTACCCC AGTCGCAATG ACCACCGTCT TAGGTAAAAA TTTATTCTGG CTATTATTTA      420
GCATGATTTC ATTTGCGGTC TTGGTTGTTA CGCTGACCTG CGCGTTAATC TGTGCTCCAG      480
GAAGAGCTGT CTGTAGTGCT GTATTTGCCC TTAAAGCCAC TGAGTCACCA ATTAACATAG      540
TGCCATCAGC AATTCCCAA CTGTTTGCAT CTGCCGTTT TGCCATCACC TTGGTCTGGC      600
CAATATTTGT TGCAGCTTGC TTCAAGCCAT TGACAGTCAA GTCTGTCTCA AACGCTCCCA      660
CTTGTGGTGC CAACAAGGTC ACCGTGCAGA CAATGATGGT CAAGATTCCT GTACCTGCTG      720
CAAGAATTGC GTGAATATAA GGCAGGGGAC GAAsGGTTTG GACAATAGGT GTGTTCTTGC      780
CTGCAATCCA AGGTTCCAAT ACATAAAATG ACAGACTGGC AAAGCCATAA GAACAAATCA      840
GAGTCAGTAA TACAGCAAGA AGATTTGATG TCAACTGTGA GAAATGATA TAGAAAGGCC      900
AATGGAAAAG ATAAACCGCA TAGCTAGTAT CCCCTAAAAA GCTGATAAT      949
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## (2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 622 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

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AAGATATATT TTTTACACAG AAGTATGCAA AAGTAAAGAG TGCAAAAAAT GGAATTAAAG      60
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1332

CGAAAATAAA AGCCGTGTAC AGGCGACCAA ACCAACGTAC ACGGCTAAGG AAAAATAACA	120
AAACTCAAGC AAAGGCAAGG CGCGTGGTTT TGTTAGGTAT TTAGCAAGGG GACAAACCCC	180
TTTGTAATA ATCTCCTCTT ATTTTATCAA AATTAGAGGA AAATGACAAC TTAATTTATA	240
AAAAGGAAAA ATGGAGGATA TAAATGGAAA TTCTGTCTAA AGAAATACAG TTACAGGGCT	300
TACAACTTCT TAAACAGACT CTTGAACTT TAGTTGAGCT AGAAAAACAA CGATCTAGTA	360
AGTTAGATTT AATTTCTCGT AAAGAATTAA TGGATCTGCT AGGTATAAGT GCTACAACCC	420
TTGATAACTG GGAGGATCTT GGTCTTAAAC GATATCAGAC TCCGATGGAT GGAGCTAAGA	480
AAGTATTCTA TCGTCCCTCA GATGTGTATT TATTTTtagc AATAAAATAG GAGTTATGAA	540
ATGAAAATTG TTACTTTCAA ACCAACTAAA CAAATAGACG ATGGGTTTTA ACTGCCAGGT	600
ATTGACATTC TATTTGTCTC AG	622

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1929 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

CGCTAACTTG CAAACAAAAG AAGAACGCAA ACTCCACAAA TCCTTTACGC AGAAACTCAA	60
TCTCATCTAC TTACCTTGCT GACTTGGTAG AGTATGTTGC AGACAAAGAC TTCTCAGTAA	120
ACGTAATTTT TAAATCAGGT ACAACAACTG AACCAGCGAT TGCTTTCCGT GTCTTTAAAG	180
AACTCTTGGT TAAGAAATAC GGTCAAGAAG AAGCTAACAA ACGTATCTAT GCAACAACCTG	240
ACCGCCAAAA GGGTGCTGTT AAGGTTGAAG CAGACGCTAA CGGTTGGGGA ACATTTGTTG	300
TTCCAGATGA TATCGGTGGA CGCTTCTCAG TATTGACAGC CGTTGGTTTG CTTTCAATCG	360
CAGCATCAGG AGCTGACATA AAAGCTCTTA TGGAAGGTGC GAATGCAGCT CGCAAAGACT	420
ACACTTCAGA CAAAATCTCT GAAAACGAAG CTTACCAATA CGCAGCTGTT CGTAACATCC	480
TTTATCGTAA AGGCTATGCA ACTGAGATCT TGGTAAACTA TGAGCCATCA CTTCAATACT	540
TCTCAGAATG GTGGAACAA TTGGCTGGTG AATCAGAAGG AAAAGACCAA AAAGGTATCT	600
ACCCAAC TTC AGCCAAC TTC TCAACTGACT TGCACTCACT TGGTCAATTT ATCCAAGAAG	660
GAATCGTAT CATGTTTGAA ACAGTTGTCC GTGTTGACAA ACCTCGTAAA AACGTGCTTA	720
TTCTACTTT GGAAGAAGAC CTTGACGGAC TTGGTTACCT TCAAGGAAAA GACGTTGACT	780
TTGTAAACAA AAAAGCAACT GACGGTGTTT TTCTTGCCCA CACAGATGGT GATGTACCAA	840

1333

ACATGTATGT GACTCTTCCA GAGCAAGACG CTTTCACTCT TGGTTACACT ATCTACTTCT	900
TCGAATTGGC AATTGCCCTT TCAGGTACT TGAATGCTAT CAACCCATT GACCAACCAG	960
GTGTTGAAGC TTATAAACGT AACATGTTTG CCCTTCTTGG AAAACCAGGA TTTGAAGAA	1020
TGAGCAAAGA ACTTAACGCA CGTCTATAAT AGAAGAAAAG AGTGGTTTGC CCACTCTTTT	1080
TACTCTCTTT ATCCATAGAA ATTGGACTCA GCCAAGACTT GTGATATAAT ATAGAAAGCA	1140
AAAAGGCAGA CGCCTAGATA ATAGGAGAAA CTATGTCAAA AGATATCCGC GTACGTTACG	1200
CACCAAGTCC AACAGGACTA CTACACATCG GAAATGCTCG TACAGCATTG TTTAATTACT	1260
TGTATGCGCG CCATCATGGT GGAACATTTC TCATCCGTAT CGAAGATACT GACCGTAAAC	1320
GCCATGTCGA GGATGGTGAA CGTTCACAAC TTGAAAACCT TCGCTGGTTA GGCATGGATT	1380
GGGATGAAAG TCCAGAATCA CATGAGAATT ATCGCCAGTC TGAGCGTTTG GACTTGATC	1440
AAAAATATAT TGACCAACTA TTAGCTGAAG GAAAAGCCTA TAAATCTTAC GTTACAGAAG	1500
AAGAGTTGGC AGCTGAACGC GAACGCCAAG AAGTAGCTCG CGAAACACCA CGCTACATCA	1560
ATGAATACCT TGGTATGAGT GAAGAAGAAA AAGCAGCTTA CATCGCAGAA CGTGAAGCAG	1620
CAGGGATCAT CCCAACTGTT CGTTTGGCTG TCAATGAGTC AGGTATCTAC AAGTGGCATC	1680
ATATGGTCAA AGGCGATATC GAATTTGAAG GTGGCAATAT CGGTGGTGAC TGGGTATCC	1740
AAAAGAAAGA CGGTTACCCA ACTTACAAC TTGCCGTGT TATCGATGAC CACGATATGC	1800
AAATCTCTCA TGTTATCCGT GGAGATGACC ATATTGCTAA TACACCAAAA CAGCTTATGG	1860
TCTATGAAGC TCTTGGTTGG GAAGCTCCAG AGTTCGGTCA CATGACCTTG ATTATCCACT	1920
CTGAAACTG	1929

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 708 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AAATTTAAGA AAAAGGAGAC ACATCATGTC TAAAAAGTA TTATTTATCG TCGGATCACT	60
ACGTCAAGGT TCTTCAACC ACCAAATGGC GCTCGAAGCT GAGAAAGCAC TTGCTGGTAA	120
AGCGGAAGTT AGCTACCTTG ATTATCAGC CTTCTCTC TTCAGCCAAG ATTTGGAAGT	180
TCCAACACAT CCAGCTGTAG CTGCTGCTCG TGAAGCAGTT CTCGTTGCGG ATGCTATCTG	240



1334

GATTTTCTCT CCAGTCTACA ACTTCTCTAT CCCTGGTACA GTGAAAACT TGCTTGACTG	300
GCTATCTCGT GCCCTTGACT TGTCTGATAC ACGTGGCGTT TCTGCCCTTC AAGACAAGTT	360
TGTCACAGTA TCATCTGTAG CCAATGCAGG GCACGATCAA CTTTTCGCTA TCTACAAAGA	420
CCTCTTGCCA TTTATCCGTA CACAAGGCGT TGGTGATTTC ACTGCTGCAC GTGTAAATGA	480
CTCTGCCTGG GCAsACGGAA AATTGGTTCT TGAAGAAACA GTCCTAACT CACTTGAAAA	540
ACAAGCTCAA GACTTGGTCG AAGCTATCAA GTAAC TAACA CTCAATAAAA ATCAAAAAGC	600
AAACTAkGAA GCTArCCGCA AGCTACTCaA gCACTGCTTT GAGGTTGTAG ATAGAACTGA	660
CGAGTGTnnA ACATATATAC GGTAAAGCGA CACTGACGTG GCTTGAAn	708

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 781 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

CTTCTTTTCT TGGAAATAGG TGTATAATAC GTTTATTAAA TTTTGTAGGA GTTGTCTATG	60
AAGAAAAGTT TTATCCATCA ACAAGAAGAA ATTTCCCTTG TCAAAAACAC TTTTACCCAG	120
TATTTGAAAG ATAAGCTAGA AGTTGTCGAA GTTCAAGGTC CTATCTTGAG TAAGGTCGGT	180
GACGGAATGC AGGACAACCT GTCTGGTGTG GAAAATCCAG TATCGGTCAA GGTCTCCAA	240
ATCCCTGATG CTACTTATGA AGTGGTGCAC TCACTTGCTA AATGGAAACG CCACACCTTG	300
GCTCGTTTTC GCTTTGGTGA AGGAGAGGGT CTCTTTGTCC ACATGAAAGC CCTTCGTCCA	360
GATGAGGATT CCTTGATGC AACCCACTCT GTTTATGTTG ACCAGTGGGA CTGGGAGAAG	420
GTTATCCCAA ATGGTAAGCG TAACATCGTT TATCTAAAAG AACAGTTGA GAAGATTAT	480
AAGGCTATTC GCCTGACTGA GCTAGCTGTT GAAGCCCGCT ATGACATCGA GTCTATCTTG	540
CCAAAACAAA TTACCTTTAT CCATACAGAA GAATTGGTAG AACGCTACCC AGACTTGACA	600
CCGAAAGAAC GTGAAAATGC GATTTGTAAA GAATTGGAG CCGTCTTTT GATTGGTATC	660
GGTGGCGACT TGCCAGATGG TAAACCGCAC GATGGACGTG CACCAGACTA TGATGACTGG	720
ACAAGCGAGT CTGAGAATGG CTACAAGGT CTAAATGGTG ATATTCTTGT CTGGAATGAG	780
T	781

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:

1335

(A) LENGTH: 846 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

CCCGCATCTT GTAGGGTTT AACGGGCACG ATTTTCATAT CCGTCTTGAT TGTTTTAGCC	60
GCTTCTAGGG CTGTTTGGTA GTTGTTTTTC GCGTCCGGAT GCGCCTTTTG TTCTTCTTCG	120
CTAACAGGGT TATCAGGAGC AAAGAAAATA GCAGCACCTG CCCTAGCCGA AGCTACAACC	180
TTCTTATCAA TACCTCCAAT GTCTCCACA TTACCATCGC GGTCATGGT ACCTGTACCG	240
GCAACAATAC GACCATTACG AAGATCTGGG TGAGCTATTT GAGTATAGAT AGCTAGACTA	300
AACATGAGAC CAGCACTTGG ACCGCCAATA CCAGCTGTTG AAAAGCTAAT TGGGACATTG	360
CTGATTACCT CTGTACGGTC AATCAAGCCG ATTCCAAATTC CATTTTGGCC ATTTTCCAAG	420
GTGATGATTT TTCCTTCTGC AGACTTGGTT TGCCCATCCT CTCATAGGT GACCTTGACG	480
GAATCCCTTA ATTTTGGAGA ACTGACGTAA TCAATCAAGT CTTTGGAAC ATCAAAGGTC	540
TGATCATTGA CTGCTGTGAC TGTATCAGAG ATATTGAGAA TCCCTTTAAA GGTGAATTA	600
TCCGTCACAT TCAAAACATA AACTCCAAAG TACTTGAGTT CGATATCCTT ACCAGCTGTT	660
TTTAGTCCTT GATACTTGGC CATATTTTGC GATGTTTGCA TGTAAGATTG ATGATTCGC	720
ATAAATTCAA CATCGGAAGA ACCACCTGTA GTCTCCTGAG CACTACGAAT ATCTGTAAAA	780
GGTGTCAACC AAGCATAAAT CATATGAGCT AAAGTGGCAT GTTGAACACC AACCGTAACG	840
AATTGT	846

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 829 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GCGATCTGCT TGGGCTTTTC CTATTACCTT ATCTAATAAA TAGGTACGCA GACTCATAAC	60
CATATAAAGT CCACCCCCCA TGGCACCGAC AAGAGCTACA TAAAAGAAGC TCCACAAACG	120
TCCACTTGGT TGGAAGAAAA ATCCTAACAG CCACTGGATG GTTCCTATTA ACAGAAACAT	180
GACTAGGGTC AGCAAACCTGA TTAAAATGGT TCGCTTCAA ATCACCTTGC GCTTGACACC	240

1336

AGTTACTTTA CAAATATCCC GATACATCAA GACGTTAGGA ATGATGAGAG CAATGGTTGT	300
TGAAATCAAA GGACCATAAC TGTGGAAGAG GCGGATGCTA GGTAAGTTCA AGACTAGCTT	360
GGCAATAGAA CCATAGATAA AATAGAGAAC GGCCTTGCGG TTGCGGAACA TGGCCTGAAG	420
CATTGGAGAC AAGACCATGT ACAAGCCTAA AATAATAGAC TGCAAAACTG CAAAGACAAA	480
TAAGCCCAGA GCCAACTAT CTGGCTTACC ATAGAAGACC GTATAAAGAG GTTCTCCTAC	540
CATAACCACT CCAACCGTTG CTGGTAGCAA GAACATAAAG AGTAGGGTGA GACTGTCCTG	600
AACGAGACGA GAAGCTGCTT TCAAGTCCCC CTTGACATAG TTTTCCGTCA AAAGTGGCAA	660
ACCAACACTC CCAATCGAAA CCCCTACAGA AATCAAAATC ATCGTGATTT TATTAGGATT	720
GGCTGAGAAA TAAGAAAACA TGACAACCAA GTCCTCATTG CTGTAGTTGG TAAACCAGCT	780
CATACTATTG ATAAAGGTCA GCTGAGTCCA AATCTGGAAG AGCTGGATG	829

(2) INFORMATION FOR SEQ ID NO: 308:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 464 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CGAACATCTT GCTGGCTGAT TCGTCTGCCG CCATCGCAGC CCCGAACACA TTGCGACCCA	60
TGGCAAGCGG GCTCAATCCG CACATGGGAT CCGTGCCAAA GCCCCGCGTG TGCATCATTT	120
GCTCATCTAG TAACGTATGA GGTTCGCCTT CGCTGTCGAT AAACCGATAT TCAATCGCAC	180
CACTGCTCGT TCTCCGCGGA GGGGAAACCG ACTGCGGTAG GATGAACTCC AGAGAAGAGA	240
GATCACGACC TACCAGGTGC GGCTCGTTGA AGCTGTTGCC GCTTAGCAGC AGGCTCGCCA	300
CCACGCATTC CCAGAACTCA ACGGGGTTT GATCGGCGTT CGCTTGCTGA CTAATAACTC	360
GGTGCACGGG ATGCGAAGTG GCCACTTCTG GCACACCGTT CTGTCTTCG TAGAGAGCAA	420
TTGGGAGGGT GGCCAGCGTT TCGGCGATGA GCGGCACGCA GGCC	464

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 982 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

1337

CCGTCATAA TGGTAATAGA TTTTATTTGG AGGTTTTTAT GTCATTTCTA TCAAAAAATG	60
GAGCAGGTAT CTTGGCCTGC CTTCTCATTT CCATCCTATC TTGGTACTTA GGAGGATTCT	120
TCCCTGTGGT TGGCGCGCCC GTTTTGGCCA TTTTCATAGG CATGCTCCTA CATCCCTTTC	180
TCTCGTCCTA TAAACAACTG GATGCTGGTT TGACCTTTAG TTCCAAGAAG TTGCTCCAAT	240
ATGCCGTTGT CTTGCTTGGT TTTGGTCTCA ATATCTCGCA GGTCTTCGCA GTTGGCCAAT	300
CTTCACTCCC TGTCATCCTG TCCACTATCT CAATAGCTCT GATTATTGCC TACCTCTTCC	360
AGCGTTTCTT TGCCCTGGAT ACAAACTGG CTACCTTGGT TGGAGTAGGT TCTTCTATCT	420
GTGGGGGTTC TGCCATTGCA GCGACAGGCC CGTTATTGAT GCTAAGGAAA AGGAAGTAGC	480
CCAAGCCATT TCCGTPATCT TTTTCTTCAA TGTCTTGGCT GCGCTCATCT TTCCAACCCCT	540
CGGCACCTGG CTTCATCTAT CCAATGAAGG CTTCCGCCCTC TTGCAGGGA CTGCGGTCAA	600
CGACACTTCC TCTGTAACGG CTGCCGCCAG CGCTTGGGAC AGTCTTTACC AAAGCAATAC	660
CCTCGAGTCT GCAACCATTG TTAAACTCAC ACGTACTTTG GCCATTATCC CTATCACGCT	720
CTTTCTATCC TACTGGCAAA GTCGCCAACA AGAAAACAAG CAAAGCCTGC AACTGAAAAA	780
AGTCTTCCCA CTTTTATCC TTACTTTTAT CCTTGCCTCT CTCCTCACTA CACTACTCAC	840
CTCTCTAGGT GTGTCCAGTA GTTCTTTTAC TCCTCTCAA GAACTCTCTA AATTCCTTAT	900
TGTCATGGAC ATGAGTGCTA TCGGTCTCAA AACCAATCTG GTCGCTATGG TCAAATCCAG	960
TGGAAAATCC ATTATCATG GA	982

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1939 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

CTAGCTGCCA ATATGATTGG GGTGCAGAAG CGCGTGATTA TCTTTAATCT TGGCTTGGTT	60
CCTGTGGTCA TGTTTAACCC AGTGCTTCTG TCCTTTGAAG GATCCTATGA GGCAGAAGAA	120
GGCTGTTTGT CCTTGGTAGG TGTGAGATCA ACTAAGCGTT ATGAAACCAT AAGGCTTGCC	180
TATCGTGACA GCAAGTGGCA GGAACAGACC ATTACCTTGA CAGGCTTCCC AGCTCAGATT	240
TGCCAGCATG AGCTGGATCA CTGGAAGGA CGAATCATTT AGGAGGAAAG CAAATGAAAC	300
GAATAGTCTT TGAACCTATT TTATCGCAA CGACCTGTA TATCTTTTTC CCGCCCTTAA	360

1338

ACCTGACCAG CTGGGAATTT CTCTTCTTCC TCTGTGGGCA TTTGTTAGTT GTGGCAATAT	420
TATTTGGCTT TGGCAAGGGG ATAAACCTTG TCAAAACGGT TCATGTGCGC CACGGTAAGG	480
CGGAAGCTGC CTTAAATCTT GAGGGTTTCA AAATCAATCG GTTAGGGAAA ATTCTGTAG	540
CTTCGATTGG AGGAATTCCT CTCTTGGCAG CTTTGGTTTc CTTGGTAACT TCCAGCATGT	600
TTCAGGCTAA AAATTATGCC AATGTAGTCA CGGTTACGGA AAAAGACTTT ACTGAATTC	660
CTAAGAGTGA CACCAGTAAG GTTCCTATCC TAGATAGAAG TACTGCTGAA AAAATTGGAG	720
ACCGCTACTT GGGTTCCCTA ACCGATAAGG TGTGCAATA CGTAGCGGCA GATACCTATA	780
CCCAATTGAC AATTGATGGG AAACCTTATC GGGTCACACC ACTAGAATAT GCAGACCCTA	840
TCAAATGGTT TAACAATCAA GCCAAGGGAA TCGGTGAGTA TATTAAGGTG GACATGGTAA	900
CTGGAATGC GGATTGTGTG GACTTGAAGA CACCAATCAA GTATTCAGAC TCGGAGTATT	960
TTAACCCTGA TGTCAAACGT CACCTGCGCT TGAAGTACCC GACCAAAATC TTTAAAACTC	1020
CATCTTTTGA GGTGGACGAT GAGGGCAATC CTTTCTATGT AGCAACGGTT TACCAAAAGC	1080
AATTTGGACT TGCTGTTCTT CGTCCTGCTT CAGTCATTAT CTTGGATGCT ACAAATGGAG	1140
AAACCAAGGA ATACAGCTTA TCAGATGTTT CAGAATGGGT GGACAGGATC TATCCAGCAG	1200
AGGAAACCTA TGAGCAAATC AACTACAACG GCAAGTACAA GGACGGTTTC TTGAATGCCA	1260
TGATTTCCAA GAAAAACGTG ACCCAGACTA CCAATGGCTA TAATTACTTG TCTATCGGTA	1320
ATGACATCTA TCTCTACACA GGTGTGACGT CGGCTAATGC GGATGAGAGT AATCTTGGTT	1380
TCATCCTTGA AAATATGCCA ACAGGAGAAA TCACTAAGTA TAGCTTGGCT TCTGCGACAG	1440
AAGAATCAGC CCGTGAATCA GCAGAAGGTG CTGTTCAGGA GAAATCCTAC AAAGCAACCT	1500
TCCCAATCCT CATCAACCTC AATGACAAGC CTCTCTACAT CATGGGCTTG AAGGACAATC	1560
CTGGCTTGGT CAAAGAGTAC GCCCTGGTAG ACGCAGTCGA GTACCAAAAT GTTATCGTTG	1620
CTACTACAGT GGAAGAGATG CTCAGCAAGT ATGCCAATAA AAACGACCTT GAAATTGACA	1680
ATGCAACGAC AGAAAGCATC AATGGAGTAG TAGCAGACCT CAAATCAGCT GTTATCAAGG	1740
GAGACACTGT CTACTTCTTT AAAGTTGATG GCAACATCTA CAAGGTCAAG GCTTCAGTAT	1800
CCGATGACCT TCCTTACCTT GAAAATGGTA AAACCTTCGA AGGTCAAGTA GGAAGAGACA	1860
ATTATCTCAA GACCTTTAAG CTACGGTAAA AATAGGTTTT TTTCAGAAAG TATATGTTAT	1920
AATAAGGTAA ATTAAGCCG	1939

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 907 base pairs
  - (B) TYPE: nucleic acid

1339

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

CCTGCTAATA GAGAGAAAGA CTAGGAGTAG AAGTAAGCCA ATTAAATAAT GAGAAAGTTT	60
CATACCCCGT CCTTTCATGT AGATTGGTA TCGAAAGATA TCTGCGGATA TAAATGTAAC	120
ATTATTTTTC TAATCTGTCA ATAAAATTTC TGACAATTTA ATAAATACAA CAAGGAGAGA	180
GCAACAAGAC TTTCTCCTTT GTTATCCTAT TCTAAAATGT TTTTACCTTA ATCTGATAAA	240
ATAATATCTT CGAGGGAGTA GCTAGCCGTC CAATCAAGAT ATTGTTTAGC TTTTGAAGCA	300
TCTGCTAGGA CACTGGCTGG GTCACCTAGCA CGTCGAGCAA CAATCTCGTG TGGGATTTT	360
TAATTTAGTA ATTCTTCAGC AGTTTAAAG ATTTCTTTGA TAGTATAGCC TTTTTTAGTT	420
CCTAAGTTAA AGATTGAGA AGAACTGTCT TCTGAAATA GGTAGTTCA TCTTTAACA	480
TGAGCCTATG CAAGGTCCAA GACATAAATG TAATCTCGAA TACATGAACC GTCACGTGTA	540
TCGTAGTCAT CTCCAAATAT TTTTAAGCTA TCATTTTGTC CCAATGCGGT CTTGTTGATA	600
TTTGGAATGA TGTGAGTGG ATTTTTCACA CGCAGACCGT TTGAAGCATC CATTCAGCC	660
CCAGCAACAT TAAAGTAACG GAAAATAACA TATTTCCAGT CGTAGCGATT GGCCATCCAG	720
TAAATCATTC GTTCGCCCAT CAGTTTGTCT TCTGCATAAG GGTGACAGG GTCGAGCAGG	780
GTATCTTCAG TCACCGGCTT GTCAATACAG TTATTTCCAT AGAGAGAAGC AGTCGAACAG	840
AACATGATTT TTTGAATGCC AACTTCAGAT AAGACTTTGA GAACTTGGTT CATACCAGCA	900
ACGTTGG	907

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CCACATAAAG GTAAATATCT TTTGTACTAT CTTGGGCATC CAAGAAAAGC AATTGGGCAA	60
TAACAGAGTT AGCCATATTG TCTTCAACCG GACCTGTCAG CATAATGATG CGGTCTTTGA	120
GAAGACGTGA GTAAATATCG TAAGAACGTT CTCCACGGCT TGTGTTTCA ATAACTACAG	180
GAATCATTCA TTTCTCCTTT TGAGTTTAA TTTTGTGGT CAAATGACTG AAGATAAGAC	240

1340

TATTATAATA TCTTGGTCAA AAAAGGTCAA ATTTTGTGCTC TGCTTTCATT AGACAGAAAC	300
AAAAACCCAA CCTCCTTTCG TGA CTGGAAA TACTTTTCCA AGTCATTCTT CTTTTCGATC	360
TTATTTTGTA CCGAACAAGC GGTCTCCAGC ATCTCCAAGA CCTGGAACGA TATAACCGTG	420
TTCGTTCAAA CGTTCATCCA AGGCTGCTGT AAAGATTTC T ACATCTGGAT GAGCTTCTTG	480
AAGGGCTTTT ACACCCCTCTG GAGCAGATAC AAGGCAGACA AATTTGATAT TTGATGCGCC	540
ACGTTTTTTA AGAGAATCAA CAGCCAAGAT TGCTGAGCCA CCTGTTGCCA ACATTGGGTC	600
TACTACAAAA ATTTGACGTT GGTCAATGTC CTCAGGCAAT TTCACCAAGT ATTCAACTGG	660
TTGAAGTGTT TCTTCATCAC GGTACATACC GATGTGGCCA ACTTTAGCAG CTGGAACCAA	720
GTCAAGAGA CCATCAACCA TCCCAGATACC TGCACGCAAG ATTGGGACGA TGGCCAATTT	780
CTTACCTGCC AATTGTTTTT GAACTGTTTT TGTAATTGGT GTTTCGATTT CCACATCTTC	840
TAGTGAAGA TCACGAAGTA CTTCATACCC CATCAACATT GCAATCTCAT CTACTAGCTC	900
ACGAAAAGCT TTTGTAGAAG TATCTGTACG ACGCAAGATT GACAATTGT GTTGAATCAG	960
TGGGTGATTA ATAACTTCAA TTTTCCCAT TTTTGGAAAT CCTTCTTTCA ATTTATTCTT	1020
CTTATTATAC CAAAAACCG TTTAAAAATC TTTCTAAACC ATTTATTTTT GATAATTTTT	1080
ACATTAGATC AGCCTCTTTA AGAGCTGTCT G TACTGTCTC AAGTGGTAAA TGGGTCAATT	1140
CTGTCCCTTT TTCTTGATAA AGGTATTGGG CGTAGTCGTC CATTCGGTAC TGGTTGATAT	1200
AAACCACGCG CTTCAGCCG ACCTGAAGCA ATTGTTTTGT ACAGTTGAGA CAAGGAAAAT	1260
GGGTACATA GGCTGTAAAG CCTTTGGGAA CACCACGCTC AGCACCTGA AGGATAGCAT	1320
TGACCTCAGC GTGAAGGGTG CGAACGCAGT GGCTTCAAT GACCAAACAT TCGTGATCAA	1380
TACAA TGCTC AGTCCCTGAC ACCGAACCAT TGTAACCAGT GGAAATAACC TTATTATCTT	1440
TTACCAGAAT CGCGCCCACT TTAGCACGTT TACAAGTGGA ACGATTCGCA ATTAGTAGAG	1500
CTTGGGCTGC AAAATACTCA TCCCAGGCCA GTCTTTTTTC AGTCATCTCT TTTCTCCTTT	1560
TTCTCTATTT TTTAAAAAAT GGTAACCTA AATCTGCAAT CTTTTCAGCT GGTACCTTCA	1620
TGCCATCCTT GATCCATTTT AGAAGGACAG AGACGATGGC TGAGCTCCAG AAGGAATGAA	1680
GATAAGAGCT GACACCTTTT GATTTCCCAT GGTATTTTTC TAGAAATTCC TGCATGGCTT	1740
GGACAAAGAT TTTTCCAGA TGGTAATCCA AGGCCAATTG AATTACTCTA GCTTCCTTTC	1800
TGGCCTCCCG GAAAAGGTGA ACCCAAACCA AATAAAGGTC TGTCTTTAAA TCGTAATGAT	1860
GCAGCTGTTT CATAATATTG TGGACAGTTC GTTTAAAGAC GCTCTCTAAA ATTTCTCTT	1920
TGGAGTCATA ATTGCGATAA AAGGCCGCAC GCGAAACACC TGCACGTTTG ACCAATTCAG	1980
AAATACTAAT CTGGTCACT TCCTTTTTTT CCAAGAGTTG CAAGAGGGCT GTTCAATGG	2040

1341

CTTCTCTGGT TAATAAATTG GATTCTTGGT TTGATTTTCT GAGATTTTCA AGAGACTTTT 2100  
 CAGAGATTCT ACGTTCAGAC ATAACATTTT CTTTCTACTT GTCACAACAG ACGGATGATG 2160  
 CTTTGTGTTTC 2170

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 539 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

ATCTGCACGA ATCAGGGCTT TCTAAGTGAC TATTTCCACC GAAATATTAT TTATATCAGG 60  
 AGGACATTCA TATGTCACGT TATACAGGAC CATCTTGAA ACAAGCTCGT CGTCTTGGCC 120  
 TTCACTTAC AGGTACAGGT AAAGAATTGG CACGTCGTAA CTACGTACCA GGACAACACG 180  
 GACCAAACAA CCGTTCATAA TTGTCAGAAT ACGGTTTGCA ATTGGCTGAA AAACAAAAAC 240  
 TTCGTTTCAC TTACGGTGTA GGTGAAAAAC AATTCCTGTA CTGTTCGTA CAAGCTACAA 300  
 AAATCAAAGG CGGAATCCTA GGTTCAACT TTATGCTTCT TTTGGAACGT CGTTTGATA 360  
 ACGTTGTTTA CCGTCTTGGT CTCGCGACTA CTCGTCGTCA AGCTCGTCAA TTCGTAAACC 420  
 ACGGTCACAT CCTTGTGAC GGGAAACGCG TTGATATCCC ATCATrCCGC GTAACCTCAG 480  
 GTCAAGTGAT CTCAGTTCGT GAAArATCAT TGAAAGTTCC AGCAATCCTT GAAGCAGTA 539

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 667 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CCGGTTTTC TCCTTCTCTA CGGCTACGAC GTGATGTATC TCTGATGATA TCCACTGTTT 60  
 CTGTAGCAGG CGTAGGTGTT TCTGGACCTG CTTGTTCTGC TTTTCTCTCT GCCGTCGTAT 120  
 AGGAAACAGC TACCCTTGTT GGGGTTTCAT TGTATTCTCT TTCAAGTTTC TTAGGTCTAA 180  
 CAGGACCTGG ACCTGGTCTT GATCCACTTT CTTCCGCTGG AGAAGAAGGT ACATCTTGAC 240  
 TTGGATGACT TGGAACACCA GGAGTTTCTC TTTGAATCTC ATCTGCTGGA GAAGCTGGTA 300



1342

CACCTTGACT TGGGTGAGTA GGCACGGTAG GAGCTTTTCT CATAATCTCC TCTACCGTTG	360
ACAAGGAATC AGCCATGAGT TCTTCAGTTG AAGGTTTCATT TGCAGGAGTG CGAACTACTG	420
CCTCATCTTC TTTCAGAACT TCATCATAGC CTTTACTTTT TTCTAAATCT CTCAGAACTC	480
GCTCTTTAAA GCGTAATTTT TCTTCTGCTC TTGACTTTTC ACTCAAAAGT TTTTCCTCCT	540
TGTTGAGAAT CCATAATATT AGAGCTGAGA AGTCCAAAAA AAGCAATCTA TGATACTTTT	600
CCTAACGGAT TTTGTCATTT CCCAGACCAT ATCATACCAT GTTTCCCCCTG CAAAGGTTGA	660
CTGGGAA	667

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

GGAAGCCAA GGTATTTTAT CGGATGAAGT TGTACTAGT TCTCACC GA TGGCTACAAA	60
AGAGTCTTCT AATGCAATTA CTAATGATTT AGATAATTCA CCAACTGTTA ATCAGAATCG	120
TTCTGCTGAA ATGATTGCCT CTAATTC AAC CACTAATGGT TTAGATAATT CGTTAAGTGT	180
TAATAGTATC AGCTCTAATG GTACTATTCG TTCCAATTCA CAATTAGACA ACAGAACAGT	240
TGAATCTACA GTAACATCTA CTAATGAAAA TAAGAGTTAT AAGGAAGATG TTATAAGTGA	300
CAGAATTATC AAAAAAGAAT TTGAAGATAC TGCTTTAAGT GTAAAAGATT ATGGTGCGGT	360
AGGTGATGGG ATTCATGATG ATCGACAAGC AATTCAAGAT GCAATAGATG CTGCAGCTCA	420
AGGGCTAGGT GGAGGAAATG TATATTTTCC TGAAGGAACT TATTTAGTAA AAGAAATTGT	480
TTTTTTTAAA AGTCATACAC ACTTAGAATT GAATGAGAAA GCTACAATTC TAAATCGTAT	540
AAATATTAAG AATCACCCCT CCATTGTTTT TATGACAGGT TTATTTACGG ATGATGGTGC	600
GCAAGTAGAA TGGGGCCCAA CAGAAGATAT TAGTTATTCT GGTGGTACGA TTGATATGAA	660
CGGTGCTTTG AATGAAGAAG GAACTAAAGC AAAAAATCTA CCACTTATAA ATTCTTCAGG	720
TGCATTTGCT ATTGGGAATT CAAATAACGT AACTATAAAA AATGTAACAT TCAAGGATAG	780
TTATCAAGGG CATGCTATTC AAATTGCAGG TTCGAAAAAT GTATTAGTTG ATAATTCTCG	840
TTTTCTTGGG CAAGCCTTAC CCAAAACGAT GAAGGATGGG CAAATCATAA GTAAGGAGAG	900
CATTCAGATT GAACCATTA CTAGAAAAGG TTTTCCTTAT GCCTTGAATG ATGATGGGAA	960
AAAATCTGAA AATGTGACTA TTCAAAATTC CTATTTTGGC AAAAGTGATA AATCTGGGGA	1020

1343

ATTAGTAACA GCAATTGGCA CACACTATCA AACATTGTCG ACACAGAACC CCTCTAATAT	1080
TAAAATTCAA AATAATCATT TTGATAACAT GATGTATGCA GGTGTACGTT TTACAGGATT	1140
CACTGATGTA TTAATCAAAG GAAATCGCTT TGATAAGAAA GTTAAAGGAG AGAGTGATACA	1200
TTATCGAGAA AGCGGAGCAG CTTTAGTAAA TGCTTATAGC TATAAAAACA CTAAAGACCT	1260
ATTAGATTTA AATAAACAGG TGCTTATCGC CGAAAATATA TTTAATATTG CCGATCCTAA	1320
AACAAAAGCG ATACGAGTTG CAAAAGATAG TGCAGAAaTwT TTAGGAAAAG TATCAGATAT	1380
TACTGTAACA AAAAATGTAA TTAATAATAA TTCTAAGGAA ACAGAACAAC CAAATATTGA	1440
ATTATTACGA GTTAGTGATA ATTTAGTAGT CTCAGAGAAT AGT	1483

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2453 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

CCTGAACGCT TTTTATATAA TATCATAAAG CCAATCTGAT TTATCAAGTG TGTCTAAGCG	60
ACGCGAATTA AAATTCATTG CATACTCCAT CGCTTCTAAA AAATCTATTT TTGAAAAGAC	120
GTTAAATCA TCTAAATTCT GACTCCAATA TAATAACAAA ACCAATCCCA TAATATCCTC	180
TGGTTGATTA TTCAATAAAT TTAAGTTGGT TTCATAAAAC CCTGGAGTTC CAAATAGAGG	240
CAACTTTTTT TCTTCAATTT GAGTTTCTTT CCTTAGGGCA TGCTCAAAGT CTATAATATA	300
AATATTATTT CTATTATCAA TAAGTATATT ATTAATGAT AAATCTCTAT AGGAAAGATT	360
ATATTGGAG TTTATTATCT CCATATAATC AATTAATGTT AAAAACCAAT CATACGAGCC	420
ACTAACCATA TTATACTCGC TTAATTTATC TGCAATAATA AACTCAAATT CCACAAAATA	480
CGAATCTTT ATGTAAAAAT CGTTAAAAAC TTTTGGAGTA AATTCCTCCT TTTCCAATTC	540
TACTAATATT TCTCTTTCAT TTATTAAACG ATTCACAGAA TCTCTATTG TAAATCAAC	600
CAACGATAAA TCACTAGCTT CTTTAAATAA AGAATAAACT CGCTTTTGAG TATTAAATAC	660
TTTATAAACT CCACCTTGG CATTTT TAGA AATCACTTCC AAAATAATAT ATTGATCAGG	720
AATAGTGTTA TATCTTGGA TATAGTAATC CCTTATTGGA ACATTCACAT TTGAAGGGAT	780
TTCTTATCT CTTTATCCT TGAAAGTGCT ATCTTTTACG AACTCCCCAT ATCTGTAATA	840
TACAACCTCG CTAAGTTGAA ATCTGAAATC TGATGGTATG TTTACACCCT TTACACCTTT	900

1344

ATACAATATT TCTAATTTGT GTAACAAACG TTGAAACTCT TTATTATCTT TTGGATAAAAT	960
TGTAATGAAT TTCCCGACTT GTGAATAACC ATTAAGCCCT GTATTTTGCA AAGAAAGTTC	1020
TTTAATGCTA ACCAAAATTT TGAAATTTAT CTTCTTCTCT CTAGAAAATA TAAAATCAAA	1080
GAATTTTTTA GCAACCAAAT TAGCATTTAA TATTGAAGCG CTCAGGTGTA TTTTAAATCC	1140
CTTAGATTGG GTGATATTAG ACGGCAAATT ATATAACCAA TGTTCATCAC TAAAATTATC	1200
ACTAATTTTA TATTCTAATA ATAAATTATG GTATGCGTCT TCTATTTTCTAG TTTTCATAGTC	1260
CAAATAGTTT AAATACTTTT CGTAATTCAT ATTAAGAAAT CTTCTCCATA AATTTTITAGA	1320
CCATCATTTA AAGCCAAACA ATTTAAAGCG TGATAATAAA TGTTGATAAT CAATGTAAC	1380
TTCACTCTCT TATTTTGTA TTTCTTCACC AATAATTTTA TGCTATATCT ATTTTCTCGA	1440
GGCAATTTAT AGGACTTCAA GATAAAACCA TAAAAGAGAT AAGTATTATA ATCTGACAAT	1500
CCAGTTTCAG AATAATTTT TAGAAAAATA TCTAGTGATT CTGATAATTC ATCCGGAATA	1560
ATTTCTTTTAA CATCGTATTT ATTTTTCATA TCGGCCACTC TTTCTTAAAA AGCTCACAAT	1620
AAAATTTTAA ATTTCTATAC AACAAATCCGA GAGTAGTCTC ACAATTTGAA CATTTCACAT	1680
CACTCTTAAT ATATAAAAA TGAATTAATC AGAAACCTCT GACTAAGATT TCCTAATTAA	1740
TTCACTTTCT ATATCATAGT AAGGAATTCT ATTATCCCTA ATTGAAAATT GAAATTTTAT	1800
GTTTTATATA TTAACAATTA TCGGGATTGT AAATCTTGTC TAACAAAATG GCAAGTGCTA	1860
CTATGTGCCC CAGAAGGCGA TGCAACGCTA TTTTGAATTG AAAGAGCATA ATCATCCATA	1920
TCATTTAAGT CACGGATTAG CAATGCTTCC TTCTCTCTTC CGACAATTCC AAATTTTCTA	1980
ATTACCTTTT CAGGATTATC AAAAAATTCT CCAACAACCT CCATATTTC TGAAGTTCA	2040
TTCAAGAAAG CTTTCATTG ACTACTCAT ATATAGCTCC TTTTCTATTA CTTTATTTGG	2100
AATCAAAACT TACTTGTTACA TTGGAAACAC CTCTATTCTA CGCTTTCATA TTGCTGCATG	2160
ACACTTTCAA AATCAAATG CTAAAAATA TTTTAAAG CTTAATTTAG ATTTAATTAC	2220
ATATATCTCA AAAAATTGTT TTGAAATTAG TAAATTAAAA TAGGTTTCTG TACTTATAGG	2280
AACTAGTTAT AAAAATTCG CCCATCATAA AATATCTATT TAAGTAAAC AAAAAATTTA	2340
TAATTTTTTG ATTTTAAAGT GACTATAATC TCCTATCTAT AAATACCATT CGCAGGACCT	2400
GGATCAATCC CTCTAGCCAT CTTATGAACT TGAGTTCCTC CAGACAGTCC CGG	2453

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1049 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CCAATTTGAA GGCTCTAAAA CAATGGAAAA GTGCTACACA GATGTGACAG AATTTGCCAT	60
TCCAGCAGTA CTCAAAAACT TTACTTTATCA CCAGTTTATAG ATGGCTTTAA CAGCGAAATT	120
ATTGCTTTTA ATCTTTCTTG TTCGCCTAAT TTAGAATAAG TACAAACAAT GTTGAACAG	180
GCATTCAAAG AGAAGCACTA TGAGAATACG ATTCTCCATA GTGACCAAGG CTGGCAATAC	240
CAACACGATT CTTATCATCG GTTCCTAGAG AGTAAGGGAA TTCAAGCATC CATGTCACGC	300
AAGGGCAACA GCCCAGACAA CGGCATGATG GAATCTTTCT TTGGCATTIT GAAATCGGAG	360
ATGTTTTATG GTTATGAGAA GAACTTTAGA TCTTTAGAAA ACCTTGAACA AGCTATTCGT	420
GACTACATTG ATTATTACAA CAACAAGAGA ATTAAGGTAA AGCTAAAAGG ACTTAGCCCT	480
GTGCAATACA GAACTAAATC CTTCGGATAA ATTAATTGTC TAACTTTTGG GGTGCAGTAC	540
ATTTTGGTGA TATATAAAAT TTGTAGGAGC TATATCTACA ATTTTATATT CCCAGTTTAT	600
GGATGTAAC TACTATATTC ACAATGTTAT CCAGTGTTTT TTCTCTAATA TTTAAGGAGT	660
GTTCGTGTTT TCGAATAAAAT TCTTCAAAGT TTAACCCGTC AACTTGTTCC TGAACAAGAA	720
AATAATCATC CACGATATAA AATTCATCAG TTAAATTAGT AGTATAACTT TTATCGGCTA	780
ATTTTITTTAG CATGTGAGCT TCATTTTTTA TATCATCAAG AGCTGTCCAT TCTCCTTCAG	840
CATCATAATT CACAAAAGGT CTTGACTGCT TGATGATTAC TTTTGGCCCC TCCGATTTTC	900
TAATGCCCCG ATAAACATTT CTTTATTTG ATCTCTTAAT AATTTTTTCC ATTTTGTATT	960
TATTTATTGC AGAGTCCTTA CTGAAACTT CACATGTGGT TTGAAAATAA ATCCTTTTTT	1020
CTTCTTCTGA AAATAAATCC ATTTCCGG	1049

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 776 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

TTAGTTGGTT AGAATCAGAA AATCGCCGAA GTGTTATTT ATTTTGAAT AAATTTAACG	60
AACCAATTAC AGCAAGAGGA GTTGCTCAAC AGTTAAAAA TTATGCTGAT AAATACAAA	120
TGAATCCTAA AGTAATTTAC CCTCATCTT TTAGGCATTT ATTTGCTAAG AATTTTATAG	180

1346

CGAAGTATAA TGATATTGCC TTGCTTGCAG ATTTGATGGG ACACGAAAGT ATAGAAACTA	240
CTCGAATTTA TCTAAGGAAA ACAGCTACTG AACAAACAAA TATTGTAGAT AAAATTGTTA	300
ATTGGTAAAA AATAACAGGT GGTCAAACCTG ACTACCTGCT ATTTTGTGA TTATGGCTCT	360
TATTATGGGA ATATACCTAT GAATTGGGTT GTTATAAAAA TAAAAGATAT TTTTCAATA	420
AATACAGGTC TTTCTTACAA GAAGGGCGAT TTAAGCATT AATAAAAGG TGTTAGAATT	480
ATACGTGGTG GTAATATTAA GCCTTTAGAA TTTTCTCTGT TGGATAATGA TTAACACATT	540
GATACACAAT TCATCTCCTC TGAGCAAGTT TATTTAAAC ATAATCAGCT AATAACACCT	600
GTATCAACCT CTTTAGAACA TATTGGAAG TTTGCAAGAA TCGAGAAAGA CTATGATGGT	660
GTGTGGCTG GTGAATGAT TTTCCAATTA ACACCATTG AAAGTGCAGA GATGATGTCA	720
AAATGTCTAT TATGTAACCT GTCTCTCCG TTATTTTATA AACAAATGAA AGCAAT	776

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 658 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC CCATTCGACC ACCAAGCGAA	60
ACATCGCATC GAGCGAGCAC GTACTCGGAT GGAAGCCGGT CTTGTGATC AGGATGATCT	120
GGACGAAGAG CATCAGGGGC TCGCGCCACC GAACTGTTTCG CCAGGCTCAA GCGCGCATG	180
CCCAGCGGCG AGGATCTCGT CGTGACCCAT GGCATGCTT GCTTGCCGAA TATCATGGTG	240
GAAAATGGCC GCTTTTCTGG ATTCATCGAC TGTGGCCGCG TGGGTGTGGC GGACCGCTAT	300
CAGGACATAG CGTTGGCTAC CCGTGATATT GCTGAAGAGC TTGGCGGCGA ATGGGCTGAC	360
CGCTTCCTCG TGCTTTACGG TATCGCCGCT CCCGATTGCG AGCGCATCGC CTTCTATCGC	420
CTTCTTGACG AGTCTTCTG AGCGGGACTC TGGGGTTCGA TGTCGACAGC CCGCCTAATG	480
AGCGGGCTTT TTTTCTCTGA GGCTGGACGA CCTCGCGGAG TTCTACCGGC AGTGCAAATC	540
CGTCGGCATC CAGGAAACCA GCAGCGGCTA TCCGCGCATC CATGCCCCG AACTGCAGGA	600
GTGGGGAGGC ACGATGGCCG CTTTGGTCCC GGATCAATTC GCGCGACCGG ATCGATCC	658

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1475 base pairs
  - (B) TYPE: nucleic acid

1347

(C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

CCGGCTTAAT TTTTAGAAAA CGTGGGCAGG GAACCTTTGT TCTCTCTCGT GGCAGCTCAA	60
AAAGAAAATT AATCGTTCCA GAAAGAGATA TCCGGGGACT GACAAAAATA TCTGAAGATG	120
CTCATTTCTAC AATTGACTCG AGGATTATTC ACTTCAAATT AGAATTTGCA AATGAATTTT	180
TAGCAGAAAA ACTACAGGTC GCTTTGCAGA GTCCAGTTTA TAATATTTAC CGCCTGCGTA	240
TTATTGACGG TAAACCTTAT GTTCTGGAAC AAAGTTATAT GAGTACCGAT GTTATTCAG	300
GTATTACTGA AGATATTTTA CAAAAATCGA TTTACAATTA CATTGAAGGA AAGTTAGGAT	360
TGCATATTGC CAGTGCTACA AAAATCTTAC GAGCTTCTTC TAGTTCAGAA AATGAGCAAC	420
ATTACTTGCA GCTCCTTCCA ACGGAACCGG TATTTGAAGT AGAACAAGTG GCTTATTTGG	480
ATAACGGAAC TCCGTTTGAG TACTCGATTA GTCGTCATCG CTATGATTTA TTTGAATTTA	540
ATTCTTTTGC ATTACGACAT TCCTCCTAGG AGAAAAATGT AAAATGAAGC CAATCTTTTA	600
CAGACTCTAG TTTAAGAAAA ATTTAAACA GGGCAAGAAG GTCCCATCTA TGCTTAAATG	660
GTTTCTCTTT TCTAAATAAG ATGGCTTTAA AAGAGTGATC GTTGTATCCA TCATGTTGAA	720
AAATATCTTC GTATAGCTTA TAGAGTAGGT ACTGAAATG TTCACCTGAT CTAATTCTTA	780
TAGTTATTTA GTTTTAAATA GTGTTTCAAA CATTCCTTACA CTGACGAGAA GTTTTTGAGT	840
CTTTCTTGT AACACATATA GTATACTGTG GTTAGAATAG TAGACTGTGA CTTCTAACAA	900
ATTGCTAGAA ATGAATTTCA ATCTCCCAAT TTATTTGTTC ATATCTTCTT TTAATATAAT	960
AAATAAATTC TAAATCATAA TCATTTAAAA AAATTTTATT TTTTATTTT CATTACGAAT	1020
AATATAGATG AAGGGGAAAG AGTATGAAAA CAGAACTGTT TCTTTTGCTA TTAGTTCAAA	1080
AGGAGAAAAA ATGAAAGTAG AAAATATTTT GTATAGGGTG GATCATCGTA AATTGTTTGA	1140
TAATATTTCT TTTGATACTT CGAGTTCAGA CGTGACATTA ATTACTGGTA AAAATGGTAC	1200
AGGAAAGTCA ACTTTACTAT AGTAGATTGA AACTAGAATA GTACACATCT ACTTCTAAAA	1260
TATTGTTAGA AATCGATTG ACTATCCTGA TCTATTTGTC CTGTTCTTAT TTCATTCAC	1320
TATATCTCAA ATTGAGTATG ACGAAGTGC CTCCCATGTC CTGGGAACGC ACTTCTTCA	1380
TATTTTTCAT ATTCTTGAAT CCATCGATAA AGACTATTGG GATGAATTTT TAAAGTTGAA	1440
CTAATCATTT TTACAGGATG AGATTACAG CAGAG	1475

(2) INFORMATION FOR SEQ ID NO: 321:

1348

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 560 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GAAATATATA TACTTCATCT TAATAGTGAG CAAGCTAAAC TTAGCATTTC ATGCCCTCAT	60
ATGGGATGTT CTTTGACTAA ATAATATGAT TATCGAGATA TATCTGGATA AATGAACTAA	120
TAACTCTGAC GCGTAGACTT ATCAAAGTCA TTGGCATACA CCACTATGAA CTCGTTGGTC	180
TGTTCAAATC CCAACACATT ACCTGAGAAG AAAGTTGCAA TGTGTGTTTT GGTGCGGGTT	240
TGAATTTAAA AAATTTGTTA TGTAGTACCT AATCTAAGGA ATTAGAACAA TGCCTCTAAT	300
TTTCTTTTAA TACACTGAAA CATTGATGAT TCTGGCTGTA TTTTGAAC AGCTCTCTTT	360
TGCTCCTGGA AAATATCTTC AGAAGTTATA TTCTCTATTC CTAACGCTAC TTGAGTTTTT	420
TTTCTAAAAT ATTCTTTTCC GTTGCCATCT TTAGAAAAAT CATAACCTTC CCTATCTACG	480
CTGTTACACA AATTAGCTAA AAAAaACTCT GGGGTTGGGA AAGGAAGATA AGAAaCGTAT	540
TTAGCCCATATA ATCTATAAAG	560

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 643 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CCGCCCCGCC ACCGCTGCCT ATCCTCGGGA GAGGGTCACC TGGAGTGAAC CTAGAACGAT	60
AGACACGGTG CGGTACGACC TCGTACTACT TTCGCCGACG GCCTCGTCCG TTGTCATCCA	120
CGAACTGATC GGACATGGGT GCGAACACTT CAGAGAAAAA ATCGTTGGAC TGCCTGTCGG	180
GCCTGAGGAA CTACGGGTGG TGGCTTTTCC GAAGAACGGC TCCGGGTTTG ATGACGAGGG	240
TACACCCTCC GAAGAGATTG TACTTGTGGA GAACGGCATT GTGAGGCACG CTGTCAGGGA	300
TCGGGCGACT GGAGGAATGG CGCCTTTTTC CGSTTTGACC AAAGTGGCAT CACATGGTGT	360
CAAACCTGGC TCAAGATGTA CGCATCTCAA GCGGAAGGG GAATCGTCAC AGGAAGGAGT	420
TACCGGAGTA CCCGCCGAAC GCACCGTTTG GATAGAGCAT TTTTCTGCAG CGAACTACCA	480
TTCAGGTCGA GCCTTTTCA GGTCTGGCCT TGCCTGGGTA GGCAGCCGAG AAGAACTCTT	540

1349

ATATCCCTTA ATGCCTTTCA CCATGTCAAT TGATATCTAC GAACTGGCCA GCTTATTTGTG 600  
GCATTTAGAC GGTCAAACGG AACGAGCAGC TAGGGTACTG TGC 643

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 780 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

GGTACCCACT CATTCTTGAT GAATTGTGAA CAGTTGCCCT TGGGTCGTTT TGCGAGTTGA 60  
AGTCAAGAAG AGGAAAAAAA CAAAAAGCAG AAATACTCAT GGCAGTAATT TCAATGAAAC 120  
AACTTCTTGA GGCTGGTGTA CACTTTGGTC ACCAAACTCG TCGCTGGAA' CCTAAGATGG 180  
CTAAGTACAT CTTTACTGAA CGTAACGGAA TCCACGTTAT CGACTTGCAA CAACTGTAA 240  
AATACGCTGA CCAAGCATAC GACTTCATGC GTGATGCAGC AGCTAACGAT GCAGTTGTAT 300  
TGTTCGTTGG TACTAAGAAA CAAGCAGCTG ATGCAGTTGC TGAAGAAGCA GTACGTTGAG 360  
GTCAATACTT CATCAACCAC CGTTGGTTGG GTGGAAGTCT TACAAACTGG GGAACAATCC 420  
AAAAACGTAT CGCTCGTTTG AAAGAAATTA AACGTATGGA AGAAGATGGA ACTTTGGAAG 480  
TTCTTCCTAA GAAAGAAGTT GCACTTCTTA ACAACAACG TCGCGCTCTT GAAAAATTCT 540  
TGGGCGGTAT CGAAGATATG CCTCGTATCC CAGATGTGAT GTACGTATG ACCCACATAA 600  
AGAGCAAATC GCTGTAAAG AAGCTAAAAA ATTGGGAATC CCAGTTGTAG CGATGGTTGA 660  
CACCAATACT GATCCAGATG ATATCGATGT AATCATCCCA GCTAACGATG ACGCTATCCG 720  
TGCTGTTAAA TTGATCACAG CTAAATTGGC TGACGCTATT ATCGAAGGAC GTCAAGGTGT 780

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 624 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

CGGGAAAAAT CAGATTGTGG GTTCAGATAT CGAATTAGCC AAGGCTATCG CAACAAAAC 60  
AGGTGTCGAA TTGGAACTAT CTCCCATGAG TTTTGATAAT GTACTGGCTA GTGTTCAATC 120



1350

AGGAAAAGCC GACCTTGCCA TATCAGGTGT TTCTAAGACA GATGAACGGA GCAAGGTGTT	180
TGACTTTTCC ATTCCCTACT ATACTGCAAA AAATAAACTC ATTGTCAAAA AATCTGACTT	240
GACTACTTAT CAGTCTGTAA ACGACTTGGC GCAGAAAAAG GTTGGAGCGC AGAAAGGTTC	300
GATTCAAGAG ACGATGGCGA AAGATTTGCT ACAAAATTCT TCCCTCGTAT CTCTGCCTAA	360
AAATGGGAAT TTAATCACAG ATTTAAAATC AGCACAAAGT GATGCCGTTA TCTTTGAAGA	420
ACCTGTTTCC AAGGGATTG TGGAAAATAA TCCTGATTTA GCAATCGCAG ACCTCAATT	480
TGAAAAAGAG CAAGATGATT CCTACGCGT AGCCATgAAA AAAGATAGCA AGAAATTGAA	540
AGAGGCAGTT CGATAAAACC ATTCAAAAGT TGAAGGAGTC TGGGGAATTA GACAAACTCA	600
TTGAGGAAGC CTTATAAGCA TCCA	624

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1237 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TCTTATGAAG CCGAAGCGTG ATTTATGGCG GATAGGTTTG GTCTGCAGAA AGTGACAAAT	60
CTAGTGCCAT CAGCGTATAT GGAATCTnTG GCTGAGAAAC AGTCCCCGGG TGAAGTACT	120
TATGAGCAGG TTTATGAGGA TGCAACGGCT TATCATCATA CCATTGATGC GAGTACAGAG	180
GAGGCAGACT TGGTTTCTCT ACGTATTGTA GAACTATTGT CTCGAAGAGG CTTTAgCTTC	240
AGTCCCTGCGA TCTTACTTGC TATTCATAAG GAGTTGTTTC AAGATATATT TGAACCCCTCG	300
ATTCCGGTAG GTCAATTTTC TCAGACTAAT ATCACAAGA ATGAACCTGT TTTGAATGGT	360
GAAAGTGTG TGTACTCTGA TTACTCCATG ATTCAAATGA CCTTGGATTA TGATTTTAAT	420
CAGGAAAAAC AAGTTGCATA TGCGACACTA ACCCAGGCGG ATATGGTTAA AAAAATCCAG	480
CATTTTATTT CAGGAATCTG GCAGATTCAT CCATTTCGCG AAGGAAACAC TCGGACGGTA	540
ACGGTATTTT TGATTCAGTA TCTTCGTGAG TTTGGTTTTC ATATTGATAA TACACCATTT	600
CAGCAACATT CCAAGTATTT TCGTGATGCC TTAGTGTTAG ATAATGCAA GATTTTACAG	660
CGACGTCCTG AGTTTTTAAC AGCTTTTTTT GAAAACTCTCT TGCTCGGTGG TCAAAATGAT	720
TTGTCTTCAG AAAAAATGTA TCTAGATTTA GACCTCGATC TTTCATAATC CTAATACTGA	780
GTAACATTG AATTTTAGGA AAAAATGAAG TAAATATTCT CACAAGAAAA CGTATATCAT	840
CAAAGTTTGG CTCTTTGTCA ATTGTAGTGG GTTGAAGAAA AGCTAAGTTC GAGAAAGGGC	900

1351

AAATTCGGC CTTTCCTTTT TGATGTTT CAG AGCGATAAAA ATCCGGTTTT TTGAAGTTTT	960
CAAAGTTTCG AAAACCAAAG GCATTGCGCT TGATAAGTTT GATGAGATTA TTGGGCGCTT	1020
CCAGTTTGGC ATTAGAATAG TGTAGTTGAA GGGCGTTGAT AACCTTTTCT TTATCTTTGA	1080
GGAAGGGTTT AAAGACAGTC TGAAAAATAG GATGAACCTG CTTAAGATTG TCCTCGATAA	1140
GTTCGAAAAA TTTCTCCGGG TCCTTATTCT GAAAGTGAAA CAGCAAGAGT TTGAAGAGCC	1200
GATAGTGATG TATCAAGTCT TGTGAATAGC TCAAAAG	1237

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TTTGATTTTT CTGAATTAGA AGAGATTGAA TTGCCTGCAT CTCTAGAATA TATTGGAACA	60
AGTGCATTTTT CTTT TAGTCA AAAATTGAAA AAGCTAACCT TTTCTCAAG TTCAA AATTA	120
GAATTAATAT CACATGAGGC TTTTGCTAAT TTATCAAATT TAGAGAACT AACATTACCA	180
AAATCGGTTA AAACATTAGG AAGTAATCTA TTTAGACTCA CTACTAGCTT AAAACATGTT	240
GATGTTGAAG AAGGAAATGA ATCGTTTGCC TCAGTTGATG GTGTTTTGTT TTCAA AAGAT	300
AAAACCCAAT TAATTTATTA TCCAAGTCAA AAAAATGACG AAAGTTATAA AACGCCTAAG	360
GAGACAAAAG AACTTGCATC ATATTCGTTT AATAAAAAAT CTTACTTGAA AAAACTCGAA	420
TTGAATGAAG GTTTAGAAAA AATCGGTACT TTGCATTG C	461

(2) INFORMATION FOR SEQ ID NO: 327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

TAACATTTAG GTACCTCTTC TTAACAAAGT TCAATAGTAA CAATTAATAT TTAAACAAT	60
ATATCAAACA TCAATGACTA GAATACTTGC ATCATCCTTC TTCCATAGA TTGGATCAAT	120
AGCAGAAGAA TTAAATCTCA TCTTAATTAA CTCTTCAAAA GTTTTATTTT GATTATTTG	180

1352

ATAGAATTCA TAAAAGCCAT CGCTCATTAA AACAATTGT TCACTAGTAA CATCTATTTG	240
ATTAATAATA GCATGGTCTA AAAATCTCTC ATCCAACGAA CCTATCCAGT ACCCACTCGG	300
TTGATTAGAT AATTTTCTGA TTTTGTGAA AATAATTTT TTATTTAAAA CACTATTTGT	360
ACCAATTGAA TCTTTTATCT CATTTTCCC TTTTCAAAT AAGTTATCTA CTCTATGATC	420
AGTTATTTCC ATTTCGTTA CTAACATGAC GCAGTCACCT AGCATCATAT ACTCCAACCT	480
TTTTCTGAA AGTTTAGCAA ATATTGGTAA GCGATAATAT AGTATATTGA AACTAGAATA	540
GTACACCTCT ACTTCTAAAA CATTGTTAGA AATCGATTTG ACTGTCCTGA TTGATTTGTC	600
CTATTATTAT TTCATTTTAC TATACTCTGT TAATTTATAT GAGTTTAAAC CGATTTTCATC	660
TTTAACCTCG AGTAAAGCAG TTTCAAATAT TTGTTTAAGA GTTTTGTATT CTTTACAATT	720
AACCGACAAA CTTTCTGATA AAATATGTAC AACTTCTGAG ACTGAATAAC CTATCTCCTC	780
TTTAGAATTA TATAAATCTG TAGCTCCACC AATAATCCAA AAATACTGAT TTTGTGAACC	840
TACAATATCC TCATTTCTA CGGAACCTCC TTGTATCGAA CAAATTTTAT TTATCTTTAC	900
CATAATACTT CAACCCTTT AGTGTCAAAA GTAAACCAAT TCCTGTCACT GTTAAGAATA	960
GTTCATAAT CTTATTCGAA CCAGTCTTTG GTAAATTTTG TTTKACATCT ACTATyCTT	1020
TAGATTTATT AATAIGATTT TCAGTTTCTC TGCCATCTCC AACTATTTTA TAGTTTACTT	1080
CTTCTGTCTT ATTATCTTGT TTATTGTCGA TCTTGTCATT CATTTGTCTA TTATCTTTAC	1140
TTGAGTTAAA CTCTCCGTTT TTCTGGTTAC TATCAATTAC ATTATTTGAA TTAGATTGTT	1200
TTCTCTCTT GTTTTTTCT TTTTCGTTT TATCACTTAA ATTATTTGTT ACAATTTTGT	1260
AAAGCCCAT CTCCGTTACA ATATTGAAAT TACCATCGCT ATCACGTATA ACAGGTTCTT	1320
TCCCATTTGC ATTAGATTG ATGAATGATA TATACTTACC GGATAAATTA TAAAATTGGT	1380
TATTTAAAC GGTTATTTA CCCTTTGAAT CCTCAATAAC AATTCCTTCT TTACCC	1436

(2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 646 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

CCGGCAGACA GGAGAAGGTG TTAAATATCA ATCTCAAATG GTTCGTCAAT GGTTCCTGAT	60
ACGTATTTTC CGTCTTCTT CCGTTGCTTG ACACACTCTG TGAGGAGATA TTCGATTGTC	120
CCATTGACTG AACGAAAGTC GTCTTCTGCC CATGATGCCA GTGCAGCGTA TAACTTTGTT	180

1353

GAGAGTCGAA GGGGGATCTG CTTTTTTTGA GCTTCAGCCA TCTTTAGTAA AGGCTTCCTG	240
TGTTGACAAT TGGTTGTGCA TCATGATTGC CACAAAGAAC GACAAGGAGA TTTGAAACCA	300
TGGCAGCTTT TCGTTCTTCG TCAAGTTCTA CCAATTCCCC TTCATTGAGC CGTTCAGTG	360
CCATTTCAAC CATTCCTACA GCACCATCTA CAATCATCTT CCGTGCATCA ATAATGGCAG	420
ATGCTTGTG GCGTTGAAGC ATAACGGCAG CAATTTCTGG AGCATAAGCT AGGTAAGTGA	480
TACGTGCTTC AAGGATTTCC AAGCCAGCAT CCTCAACACG ACTTTGGATT TCTTCACGAA	540
TACGGGTAGC AACAAATTCG CTAGAGCCAC GGAGACTACC TTCATCTGCG TGCCCATCAC	600
CCGGAGTATC CACATTAGGA GACACATCGT AAGGATAGAT GCGGAC	646

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1653 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

GTTCGAGGTG CAGTAGGTGT TACTTCAGAT ACATTTGAAC GTGCAGAGGC TCTTTTGTAG	60
GCAGGAGCGG ATGCGATTGT TATTGATACT GCACATGGTC ATTCTGCAGG TGTCTGCGT	120
AAAATTGCCG AGATTCGTGC TCATTTCCCA GATCGGACTT TGATTGCTGG AAATATTGCT	180
ACTGCTGAAG GTGCACGTGC CCTTTATGAA GCGGGTGTAG ACGTTGTTAA GGTTGGTATT	240
GGACCAGGTT CTATCTGTAC TACTCGTGTG ATTGCTGGTG TTGGTGTTC GCAAGTAACA	300
GCTATCTACG ATGCTGCAGC TGTTCGCGC GAATATGGTA AAACGATTAT TGCTGACGGT	360
GGGATCAAGT ATTCGTGAGA TATTGTAAAA GCACTTGCTG CAGGTGGAAA TGCTGTTATG	420
CTTGATCTA TGTTTGCTGG AACTGATGAA GCTCCAGGCG AAACGAAAT CTCCAAGGA	480
CGTAAATTC AACTTACCG TGGTATGGGA TCAATTGCTG CTATGAAGAA AGGTTCAAGC	540
GACCGTTATT TCCAAGGTTG TGTCATGAA GCAAACAAGC TTGTTCCAGA AGGAATTGAA	600
GGTCGTGTTG CTTATAAAGG AGCGGCAGCT GATATTGTTT TCCAAATGAT TGGTGGTATT	660
CGCTCTGGTA TGGGTTACTG TGGTGCAGCT AACCTTAAAG AACTACACGA TAATGCTCAA	720
TTTATTGAAA TGTCGTGTC TGGTTTGAAA GAAAGCCATC CTCATGATCT GCAAATTACT	780
AATGAGGCAC CAAATTATTC TATGTAAAA ACAATGAAA GAACTCCAGT GAAAACAGGA	840
GTTCTTTTAC AATGTGTCA ATTTCCATTT ACAGCAGCTT TACCATCCTG AATAGTGAAG	900

1354

ATACTTAGAT TTTCTGGCAG ATTTTGAAGA TGGTCTAAGC TTGTTGTTGT GATAAAGGTT	960
TGGATTGATT GAGAAATCGT TTCTAATAAT TTTAACTGTC TAGTGTGTC AAGTTCACTC	1020
ATCACATCGT CAAGCAGTAA TATAGGAGAT TCTGTGGTAA TGCTTTCCAT TAATTCGATT	1080
TCTGCTAATT TTATCGAGAG GACGAGACTA CGATGTTGAC CTTGGCTTCC GAAACTAGCA	1140
TCCATCCCAT TTATATAAAA AGAAATGTCA TCTCGATGAG GACCGACACC AGTATTCTTT	1200
TTAAATAAAT CTCTGGATCT ACTTTTTTCT AAAGCAATTT TGAAAGATTC GGATAAGTTT	1260
TGTTTGTCAG TTATATTGAC AGAAGATTGA TAGGATATTG ACAACTCTTC GATCTGATTA	1320
GAGAGTTCAA AATGTTTCTT ACGCCCAAAT GATTCTAGTT TTTTATGAA ATCTAAGCGG	1380
TGATTCATTA CACGACATCC ATAATCAACT AGCTGATCAT CTAACACAGA AAGGAATGTT	1440
TCATCTATTT TTTGAGCTGA TTTTAGGTAA GTGTTTCTTT GCTTTAGGAT GTGGTTATAA	1500
TTGGTTAAGT CAGATAAATA GATTGGCTTA ATTTGCCCAA GTTCCATATC AATGAATTTT	1560
CGTCGAATCG AAGGTGCTCC TTTAATTAGT TGTAAATCTT CAGGAGCAAA TAAGACAACA	1620
TTCATGTGTC CTACATAATC TGAAAGGCGT GCC	1653

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GAAACACTGT ATTTCAAAGC ATTTTGTGTT AGTTTAAAT TACTCCCATT CTTCTTTTCC	60
AAACGTACAA TATATCCAAA ACCATTCAAA ATACTAGATT CTATTTTSTA TAATATCACT	120
AAATCCACCT AATTATAGGA CGTTTTCAGA TTTTATGTC CAGTCCCAGT ACCGAGAGAA	180
TATTGTTTTA ATATAATATC TCTTTTGTG TTCTAAGCTC TTAAGAGCAA AAGAACAAGT	240
AAAGAGTCAA GACAAGGATA AAAAGTCCAT ATTAGGGCAA ATAAAAAGCT TTAAGACAGA	300
TGACAAATCT AAGTCAATA AGAAAGACCA TAGCAAAGGT GCAGAGAGAT AAATATTGGC	360
GGTCTTCGGA CTGCCTTTAT TTTTATATCC ATTTTCAAA TCAAATTTAT TCAGACTATA	420
TATGCACATA TACACTTAAA TTCATATAAA AACATGGCTT GTAAAAAAT ACTTTAATCA	480
CAATAATCGC ATTTAAATTT GTGATGTTTG CAAGCTAAAT TACGGACTTC ACTTGAAGT	540
TTTCCCTTGT ATCTTTTATA ATAGATAGAA AATTGCTGG CAGATGAATA TCCAACAGAT	600
TCTGCTATCT CTTTATAGG TAGTTCAGTG TTTAAAGAA GAGTTTCAGC TACATTCATT	660

1355

CTTTTCTTT GAGTGACTC TGTAATGCTT TGACAATATT TTTCCTTAAA TAAATTTTTT	720
AATTAGTAC CACTCATTTT AGATATTTTT TCAAGCGTGC CTTGATTAC ATTCGTTGCA	780
AAATGATCAT CTAAGAATCT TGCTACATCT TCAAGTGCTT TATCATCATC AATTTC AATT	840
TTATATTTTT TTCTATTTAA GTATGTGTCA ATTACTATAC TTATCCATTC ATTTGCCTTT	900
GCTTTAAAGA AAAAATCAGC GGCAGGAGCG TCCATCTTAC AATTTAATAT TTCCATTGCC	960
ACTCTTTCTA AGGCCCTTGT AAGTATTATT TGATTTCGGTT GAAGCAAGGT TGAATAAAAA	1020
GATTCTGGAT TAATGTTAAT AGATGCTAAA TGTTTTTCTA TTAGCTCTTT TTAAAAACCT	1080
ATGGAAACAG CAAGATAACA ACAATTCTCG TGTAATAAAA AAACAAAATT ATCTTTTATA	1140
TTATCAAAAT CAAAAGTACA TAGAGAGTTT GCGGTAATAG TTTGATACCG ATTAACTTT	1200
TCTCCGTTTG CACTGACAAT GTAACCTGAA TAAATTGAAA CATAGTCTGA CATACTATAA	1260
GTGCTATTTT GAACACTTC CTCTTTGATA TAAAAATCAT GTATATCGAT AATGAAGATG	1320
CCTCCTTCAT AAAACCGGTA	1340

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 607 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

TATGTTCTG ATGAGTTTTT AAGTAGGAAA AACGTGCTAA CCTCTCAGAT TTTGGAACCT	60
GTAAAAGAAA CTCTTTTTC ACCCGTAGTA GTTGATAATG GGTTCGATCC GGCCTTATTT	120
GAAATTGAGA AAAACAATT GCTAGCAAGT TTAGCAGCTG ATATGGATGA TTCTTTTAT	180
TTTGCACATA AAGAATTGGA TAAATTGTTT TTTCATCATG AACGCTTCA ATTGGAATAT	240
AGTGATTAC GAAATCGTAT TTTAGCTGAA ACTCCACAAA GTTCTTATTC TTGTTTCCAA	300
GAATTTTTC CCAATGATCG AATAGATTTC TTTTCCTAG GTGATTTTAA TGAGGTGAA	360
ATTCAAAATG TATTAGAATC ATTTGGCTTT AAAGGTCGAA AAGGAGATGT GAAGGTCAG	420
TATTGTCAAC CTTATTCTAA TATCCTTCAG GAAGGTATGG TTCGGAAAAA TGTGGGACAA	480
TCCATTTTGG AATTAGGTTA TCATTACTGT TCTAAATATG GTGATGAGCA ACATTTACCC	540
ATGGATTGAA TGAATGGTTT ACTTGGTGGA TTTGCTCACT CTAAGCTCTT TACAAATGTC	600
CGGGAAA	607

1356

## (2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 900 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

TTAAAAATACC GAATTTTGTT TTGTCCTCTA TTTCAACATT GTGAATCGCC TCAGGCAGAG	60
AACCGATACT AAAGATATAA CCAAATAGT TGTCAATTGC TTTACCGATA TCAATCTTAT	120
TGGTTAAATC AAAATCCAGT TCGTCAATTG CGCCATCGAT GTCTTGATTG ATTTCCAAAA	180
GTTTTGTAAT GAGGTTACCC GTACCGCCTG GGATAATCCC TAACTTAGGA ATGTAGTCTC	240
TCTCATCAAT ACCTGAAATG ACTTCATTGA CAGTTCCATC TCCACCAAAC ACAACCACTG	300
CATCATACTG CTCACGAGAA GCTTCTTCAG CAAAATCTGT TGCATCCAGC GCTTTTTCGG	360
TAATTTTGGT TTCAACATAT TCAAAGTATT CTTTTCGCTT ATTCTCCAGC TTTTCTTTGT	420
AATCCAAAGC CTTCTCGCCA CCAGAAGTAG GGTGATAAT TACCATTCGT TTTTTCATTG	480
ATTTATCCT TAATTTTAAA CAGAAATGTT TACATTCGT CGTATGCAAG TAAATGTAAT	540
CCTATTATAC AATGAAAATA CAGAAAAGAG AAATCTGACG TACTGGAGAT TAATACGCTT	600
TTATTCTATT TTCCCATCGC CTAACATACAT CCTTAAAGG TTCATCCAAG TAAGAATAGG	660
CCTTATCCTT GATCCAATCA GGAATACCGT AAGCTGCCTC TGCTAwGCTA CAAGTGATTG	720
CTGCGAGAGT ATCACTGTCTG CCACCAAGTG AGATGGCATT TCTTATCGCA TCTTCGAAGT	780
CTCTACTTTC AAGAAAGGCC ATAATGGCTT GAGGGACAGT TTCCTGACAT GTTTCGTTAA	840
AACGATAGTT AGGACGGATT TCATCTAAAG TTTGAGATAG ATTGTAATCG TATTCTTTTT	900

## (2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 533 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

CCTTCTGGC ACACTGGTCT TGAATACGG CAAAACCTCT GAAAATATCT ATGCTGGAAT	60
GGACGAGGAA TACCGTCGTT ATCAGCCTGC CATCATCACT TGGTACGAAA CAGCCAAACA	120
TGCTTTTGAT CGCGACAGA TTGGCAAAAT ATGGGTGGAA TCGAAAACGA CCTCAAGGGC	180

1357

GCTCTCTACA GCTTTAAATC CAAGTTCAAT CCGACCATTG AGGAATTCGC TGGTGAGTTC	240
AACCTGCCAA CTAATCCTCT TTACCACCTC TCCAATCTGG CCTACACTCT CAGAAAGAAA	300
CTGCGCAGaA GcATTAAACAG AAAGGAAGCC TATGACCTTT AACTTCTCA GCCAAGAAGA	360
ATTCATCCAG CATACCTCAG CTAGATCCCA ACGCTCTTTT ATGCAGACCG TAGAAATGGC	420
AGAGCTGCTG AGCAAGCGTG GCTTCAGTAC CCACTATGTC GGCTACACTG ACCCACAAGG	480
GAAGGTAGTG GTGTCAGCTG TCCTCTACAG CATGCCTATG ACTGGTGGCC TTC	533

(2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 544 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

CCAGCAAACCT AGGAAGCTAG CCGTAGTTGC TCAAAGCACA GCTTTGAGGT TGTAGATAAG	60
ACTGACGAAG TCATGTACAA AACACTGTTT TGAGGTTGCA GATAGAACTG ACGAAGTCAC	120
TCAAACAACT GTTTTGAGGT TGCAGATAGA ACTGACGAAG TCACTCAAAA CACTGTTTTG	180
AGGTTGCAGA TAGAACTGAC GAAGTCanna ACCACACCTA CGGCAAAGTG AATCTGAAGT	240
GGTTTGAAGA GAGTACAACT TGTCTTTTAG AAAAGGAGCC TATAATGAAA GTCTTTCAGC	300
ATGTAAATAT CGTGACTTGT GATCAAGATT TCCATGTTTA TCTTGATGGA ATCTTAGCAG	360
TCAAGGATTC TCAAATCGTC TATGTCGGTC AAGATAAGCC AGCGTTTTTA GAGCAAGCTG	420
AGCAGATTAT AGACTATCAG GGAGCTTGA TTATGCCTGG TTGGTCAAT TGTCACACCC	480
ATTCTGCAAT GACAGGCTG AGAGGGATCC GAGATGACAG CAATCTCCAT GAATGGCTCA	540
ATGA	544

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

CCAGGAACTC AAATGTAAGT AGGGGTTCCCT TTTTGTATA TTTTCAAAT AACGCCTCTA	60
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1358

CACTATTTGT AGCAAATTCA CCAACTACAG TTGTATCTTA GTTAAATAA GTTAGAATAT	120
GTAAGTGAGT ACCAGATATA CCAAGACATC GTCACCACTT AAGGTATATT CAAAATACAA	180
AAGTTGACCA ACTAGATTTC TGAATATCCT TATATATCCA TTCTTAAAT TGGTTTAAAT	240
AGCGTAGTCT TTAAACTAG TTTGAGAAT CCAAAAAATC TTCCTACATA TGTAAGAAGA	300
TTTTTTAGTT CAGAATGATT AGATTTAGCT AATGGATACC TATCCTACC	349

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1206 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

CTCCGATAAC CACACCAGCA ATGGAAATAA TTCCATCGTT AGCATCAAGA ACACCCGCAC	60
GCAGGATATT TAAACGACCT GCAAAATTTG AATCAATTTC GTGATTGTGTT TCTGACGCTA	120
AATTCAAGT TCAAGTTAGC CATCAAGAAG TCTTCTCTGG GTGACTTGTA GTCCAAGCAT	180
TTTTTAGGAT AGTTGTTAAT CCACTTTTCG ATGAATGCGA CTTCTTTGGG AGTCATTTTC	240
TTGGTTCCTT TAGGTAACCA TCTACGAATG AGCCTGTTGT GATTCTCATT AGTCCCGGG	300
ATCCTCTAGA GTCGACCTGC AGGCATGCAA GCTTGGCACT GGCCGTCGTT TTACAACGTC	360
GATGACTGGG GAAAACCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTTT	420
CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG	480
CCTGAATGGC GAATGGGGCC TGATGCGGTA TTTTCTCCTT ACGCATCTGT GCGGTATTTT	540
ACACCGCATA TGGTGCACTC TCAGTACAAT CTGCTCTGAT GCCGCATAGT TAAGCCAGCC	600
CCGACACCCG CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC	660
TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAAGTTT CACCGTCAATC	720
ACCGAAACGC GCGAAACGAA AGGGCCTCGT GATACGCCTA TTTTATAGG TTAATGTCAT	780
GATAAGGATG GTTCTTAGA CGTCAAGTGG CACTTATCGG GGAAATGTGC GCCGAGACCC	840
TATTTGTTTA TTTGTCTAAA TACATTCAAA TATGTATCCG CTCGTGAGAA AATAAACCTG	900
ATAAATGCGT CAATAATATT GAAAAATGAA GAGTATGAGT ATTCTACATT TCCGTGTCGC	960
CCTTATACCC TTTTGTGCGG CATGTTGCCT TCCTGTTTTT GCTCAGCCAG AAAACGCTGG	1020
TGAAAGTTTA AGATGCTGAA AAATCATTTG GGTGCACAAC TGGGGTTACA TCCAACCTGA	1080
ATCTCCAnCA GCAGTTAAGA TCCTCTGACA GTTGTACAG CCGCAAGAAC TATTCCTCAT	1140

1359

GAATGAGCAA CTTTAAAAAG TCCTGCCAAT GTTGGGGCGG TAATAATCCC CGTGTGTAG 1200  
 GCCCCG 1206

## (2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 813 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CTGCTCAACT CAGACAGTCA AATTTCTGAC TTTACCAAAA GAACCATCAA AAAAGTTGCT 60  
 GAAAAAGGCC ATCAGGTTAT TATTACGACA GGTGCGCCTT ACCGTATGTC AAAAGATTTT 120  
 TACCGTGAAC TGGGCTTAGA CACTCCTATG ATTAAGTTCA ACGGATCCCT TACTCATTTA 180  
 CCAGACCAAG TTTGGGATT TGAAGAGTGT TTGACTGTAG ACAAAAAATA TCTGCTAGAT 240  
 ATGGTTCAAC GTTCAGAGGA CATTCAAGCC GATTTTATCG CTGGAGAATA TCGTAAAAAA 300  
 TTCTACATTA CAAATCCCAA TGAAGAAATTT GCCAATCCCA AACTATTTGG TGTAGAAGCT 360  
 TTCCAGCCTG AAGATCAATT CCAGCCTGAA TTGGTGACCA AGGACCCTAA CTGTATCCTC 420  
 TTGCAGACTA GAGCCAGTGA CAAATATTCC TTGGCAAAAG AAATGAACGC CTTCTACCAG 480  
 CATCAACTTT CTATCAATAC CTGGGGAGGT CCGCTCAATA TCCTTGAATG TACCCCAAAA 540  
 GGTGTCAACA AGGCCTTTGC TTTGGACTAC TTGCTCAAGA TAATGAATCG TGACAAAAAA 600  
 GATTTGATTG CCTTTGGAGA TGAACACAAT GATACCGAAA TGCTCGCTTT TGCTGGGAAG 660  
 GGTATGCCA TGAAAAATGC CAATCCAGAG CTACTCCCTT ATGCAGATGA GCAAATTTCC 720  
 CTTACCAACG ACCAAGATGG GGTGCGCAAA ACCCTACAAG ACTTATTCTT ATAACCTATA 780  
 CTGATACTCA ATGAGGGGCA AAGAGCGAAC TTA 813

## (2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 683 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

CCTAGATAAA TGATATAATT CTATTATTGT TCGTAAAAAT TAAAAGGAGA TTGATGATGG 60

1360

ACAAATTATT TAAACTAAAA GAGAACGGTA CAGACGTTTCG TACAGAGGTT CTCGCTGGTT	120
TAACAACCTT CTTTGCAATG AGCTATATTC TCTTTGTAAA CCCACAAATA CTTTCACAAA	180
CAGGAATGCC TGCTCAGGGC GTCTTCCTAG CGACGATTAT TGGTGCAGTA GCGGGTACCT	240
TGATGATGGC TTTTATGCT AACTTACCTT ATGCCCAGC GCCAGGTATG GGACTCAATG	300
CCTTCTTTAC CTTTACAGTT GTATTCGGGC TTGGTTATTC TTGGCAAGAA GCCCTAGCTA	360
TGGTCTTCAT CTGTGGGAT ATTTCATTGA TTATTACCTT GACAAATGTT CGTAAAATGA	420
TCATTGAATC GATTCCCAAT GCTCTTCGCT CAGCTATTTTC AGCTGGTATC GGTGTCTTCC	480
TTGCCTATGT AGGGATTAAG AATGCTGGAC TTTTGAAATT CACGATTGAT CCAGGCAACT	540
ATACTGTGT AGGAGAAGGG GCTGACAAAG CTCAAGCAAC GATTGCAGCA AACTCTTCAG	600
CAGTCCAGG ATTGGTCAGC TTTAATAATC CAGCTGTTTT AGTGGCTCTT GCAGGACTTG	660
CCATTACTAT CTTCTTTGTC ATC	683

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 852 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CTACTTTACA TGGAAGTAGT CACTGAATTC CAGTTAGAAA TTACTTTGTA ACTACGTTTT	60
GAGGAGGAGT AAAATGCTTT CCTACGTTTCG ATATTACCCA CTAGCGATAG CTAAATTAAT	120
GTGTCGTGTC TCTCCTAAAA TCTGCTGATT TATTACTGAC TAATACAGGA GGTTTTTTTT	180
ATGgACAGAC AATCATATCT GCTATTGGTG TTTATATTTT CACCAGTATC GATTATTTAA	240
TTATTTTAAAT TATTTTATTT GCACAGCTAT CACAGAATAA ACAGAAATGG CATATTTATG	300
CGGGGCAATA TCTAGGCACA GGCTTACTTG TAGGGGCGAG TTTAGTTGCT GCTTATGTCG	360
TTAATTTTCGT GCCTGAAGAA TGGATGGTTG GATTGCTTGG TTTAATCCCT ATCTATTTAG	420
GGATTTCGCTT TGCAATTGTT GGAGAAGATG CGGAAGAAGA AGAGGAAGAA ATTATTGAAA	480
GATTAGAACA AAGCAAGGCA AATCAACTGT TTTGGACAGT TACATTGCTG ACAATTGCGT	540
CTGGCGGAGA TAATTTAGGT ATCTATATAC CTTATTTTGC TTCGTTAGAT TGGTCACAGA	600
CCCTCGTGGC CTTGCTTGTG TTTGTAATCG GCATAATTAT CTTTTCGAG ATTAGTCGGG	660
TGTATCCTC TATTCGGTTA ATATTCGAGA CAATTGAAAA ATACGAGCGA ATCAATTGTGC	720
CCTTAGTATT CATTCTACTT GGACTATACA TCATGTATGA AAATGGCAGC ATAGAGACTT	780

1361

TTCTGATCGT GTAGATTTTT TTGTTTCACT AGGGATTAG CCCGAGCTCA AATCAGCTCT 840  
CTGATTTTCA GA 852

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 754 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

CCGCACAAAA GCGCATAGTA TCAAGATTCT ATAAAGCCTT GATACTATGC CTTTTTAATC 60  
GATAAATAGT TAGTCTTTTT TAAAGACCGG ATCTTTCAAA CTCTGCATAC TGGCATTGAT 120  
CACCGCGCCT AGGATAACAA TTTTAGCAAT CAAGATAAAC CAAAACA'TCA TAACAACAAG 180  
AAGAACGGAA CCTAAAATTC GGACATCCAC CAAATGATGG ACATAGTAAT TGAGATAACT 240  
AGAGAACAGA GTTAGTAAAC CTAATATCAC TAAGAGAACA AAGGCACTGC CTGGTAGGGT 300  
ATAGCTAATT TTCCTGTTAG ATAGATTGGG AAGAAAATAA TAAAGCATGA CCAAGATAGC 360  
AAAGAGGAGG CCGTAAATCA GAGGACCTGC CAACCTTGT AAAGCCTGAT AGATAATGCC 420  
ATCTTTTGTC CAATAATGAG CAAGTAAAGC CAAATCATC TGACCAAATA AGATCAAAAA 480  
CAAGGCAAAC GCAAAGAGGA GCTGCAACCA AACTGACTA GGAGACTTAG CATCTCATGG 540  
GAAATAAGTC CAGACTCTT TTCGACGCCA TAAGCCTTGT TAAAAGCTTT TTGCAAGAAA 600  
TTCATAGATT TTGAAAACT CCATAACGCC GATAAACAG AAAA'ACTCAA TAAACCTGTT 660  
GAAGGTTCGG TCAAGACTTC TCTGGCTATT TTTCCACAC CTTCATAGAG GCTTGGGGGG 720  
CAGACGTCTT TCATAAAGCC CAAAATTCT C'CCA 754

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GGGGATAACT CTAGGAGTAC CGCTATTACT CGACTTAATG AGTGCACAAG AAGTCAGGAT 60  
TTTTATGCAG GTTGGGCGCT TCATCAGACA GGGAAGATTT ACAGCGACTA TTATGGAAGT 120

1362

CAAGGTTTGC TTTATTATTT GCTGACTTAC GTGAGTCAGG GCGGATTTTT CTTTGCCATC	180
TTTGAGTGGT TAGCCTTGGT AGCAGGAGGA TTTTTCCTTT TTAGATCAGC GGACACCTTG	240
ACAGAGCAAG GAGACCAAGC TGGACATCTG GTGACTATTT TTIACATGCT AGTTACAGGT	300
CTTGCTTTTG GTGGAGGCTA TGC GACTCTT TTAGCGCTTC CTTTCCTTAT CGCAGCCTTT	360
AGTTTAGTTG CGGCTTACCT AAGCAATCCA AGCCATGATA AGGGATTGT ACGGATTGGG	420
CTAGCTTTGG CAGGCGGATT TTTCTTTGCT CCCTTATCAT CGCTCCTGTT TATTGCTGTA	480
GTGAGTTTAG GCTTGTGGT CTTTAACCTT GGGCATAGAC GCTTTGCGCA TGGGTTTAT	540
CAGTTCTTG CAGTGGCTTT AGGTTTTTCA CTTGTCTTTT ATCCAACGTC CTACTATAGT	600
GCTGCAACAG GAAGTTTGG GGATGCGwTT AGTGGTATTC GTTATCCTAT TGACAGTATT	660
CGCTTTGATT TTACTTCTAA AATTTTAGAG AATATGTTTT TTAAAG	707

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 762 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GGATTTTGAA AAACCATACC GATTTGACGA CGTATATTCC AAACATTTTC CTCAGTCAAA	60
CGTTGGCCAT CAATTACAAT CTCTCCGAT TCTGCTTCCA GTAAGCCATC AATTAATCGA	120
ACCGTCGTTG ATTTACCACT ACCATTATGC CCTACAATCG AAAGCCATTC TCCACGTTTC	180
ACGTGAAAgt AATATCCTTC ACATCGTAGT AGTTCTGATT TTCTTTATAG CGAAAAGAAA	240
GATTTTTTAC ATCAATTATT GATTTCAATT CGAACCAAAT GTCCCTTTAA ATACATAGGC	300
ACTACCCTTG AAATAGTCAT AGCCAGAGTA GATAGTGAAA AATAAGGCTA CATAAAGTAG	360
AACTTGACCA AGCAAAGTCC AATGTAATAG CAAGAAAATA ATGGCAAACA TCTGACTAAA	420
AGTTTTAATT TTTCCAGGCA TTGCTGCTGC TAAAATTGTT CCACCAGTTT CAACCAATAA	480
AAGCCTTAAA CCTGTCACAG CTAACACAG ACAGATAATC ACTGCAACAA TCCAAGCCGG	540
AGCCATACCT AACTCAATCA ACATAATAAA AGCCGACATA ACTAGTAACT TATCCGCCAT	600
AGGATCTGCA AATTTACCAA AATTACTGAC CACATTCCAT TTACGAGCTA AATATCCATC	660
TAAATAGTCG GTAATACTGG CAACAGCAAA GATAATAGCT GCAACTATAT GACTCTCTAT	720
CGAATTTCCCT ATCGTTAAAA TAAAGATAAA AATAGGTATA AA	762

(2) INFORMATION FOR SEQ ID NO: 343:

1363

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 482 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

```

CTTTTGATAC ACTTAACTA TGAATACAAA TCTCAAGCCC AAACCTCAGC GTTTTGCTTC      60
TGCGACTGCC TTGCGCTGTC CTATCTGTCA AGAAAATCTG ACTCTGTTAG AGACTAATTT      120
CAAGTGCTGC AACCGTCATT CTTTGACTT GCGGAAATTT GGCTATGTCA ATCTAGTCCC      180
TCAAAATCAAG CAATCTGCTA ACTACGACAA GGAAAATTTT CAAAACCGTC AACAAATCCT      240
AGAAGCCGGC TTTTACCAAG CTATCTTAGA TGCTGTATCT GACTTGCTTG CAAGCTCAAA      300
AACTACCACA ACAATTTTGG ATATCGGTTG TGGTGAAGGA TTCTATTTCTC GCAAACCTACA      360
AGAAAGTCAC TCTGAAAAAA CTTTCTATGC CTTTGACATC TCCAAAGATT CAGTCCAAAT      420
CGCGGCTAAA AGTGAACCCA ACTGGGCAGT CAATTGGTTC GTTGGCGACT TGGCACGACT      480
TC                                                                                   482

```

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 520 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

```

TTTATTTTTA TAAAGTCAAT ACCTGTCTTT ACTTTTCTT AAAAAAAGTT TATTATGTTT      60
TTTAAGGAGG TGTA AACAT GAAAATAAAT AATAAACTCG TTGGAGAACC TATTCAAAAT      120
ATCCGTTTAA GCCATGGCGA CTCTATGGAA AAATTTGGAG AAAAATTTAA TACTAGCAAA      180
GGTACAGTTA ACAACTGGGA AAAAGGTCGC AATTACCAA ATAAAGAAAA CCTACTAAAA      240
ATTGCATCTA TTGGA AAAAT GACTGTTGAA GAGTTACTCT ACGGCGATTA CAATACTTAT      300
CTACACTTAA AGATTATGGA TTTAGCTCCT GAATGTATAA AAAATTATGA TGAGTATAAC      360
TCTTTACACG ATGATATAAC AAATAAGCG TTACAGATCG CTCAAAATAC CATTTCTAAG      420
ATTGATTATC AAATTCAGA CGAAACGATC AAAAAATTTA TTGATTTAGC TATCGAACAA      480
TCGAGAGATT TGCAAGGAAA TTTGTTGAAA AATAACGGGT                                520

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1364

## (2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1003 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```

GCATCAAATC CGCCATCAAA GAAGTTCTCT GGATTACCA AGACCAGTCA AATAGCTTAG      60
AAGTGCTTAA TGACAAGTAC AATGTTCACT ACTGGAATGA CTGGGAAGTT GGAGACACGG      120
GAACCATTGG TGAGCGCTAT GGTGCCGTTG TTAAGAAACA CGACATTATC AATAAGCTTC      180
TCAAACAGTT GGAACCAAT CCTTGAACC GCCGCAATAT TATTTCGCTC TGGGATTACC      240
AAGCTTTCGA AGAAACAGAT GGGCTGCTCC CGTGCGCCTT TCAGACCATG TTTGATGTTT      300
GGCGTGTTGA TGGGGAAATC TATCTGGATG CGACCTTGAC CCAGCGCTCC AATGATATGC      360
TGGTGGCCCA CCACATCAAC GCTATGCAGT ATGTGGCTTT GCAGATGATG ATTGCCAAAC      420
ATTTTGCTG GAAGTTGGG AAGTTCTTCT ACTTCATCAA CAACCTCCAT ATCTATGATA      480
ATCAATTGA ACAAGCTCAG GAATTGCTCC GTCGGGAGCC GTCAAAGTGC CAACCACGCT      540
TGTTTAA TGTTCCTGAT GGGACTAATT TCTTTGATAT CAAAGCAGAA GATTTTGAGT      600
TGTTGGATTA TGACCCTGTT AAGCCACAGT TGAAGTTGA CCTAGCTATT TAAAAGAATA      660
GAAAAAGAA GTTGAGAATA ATCCCAACTT CTTTGTGTTT TTAACGTGAT ACGCGGCGAC      720
GAGCTGCTTT TTTACGGTTT TCTTCGATGA AAGCTGCTTT TTGCTCTTCT GGTTCGATTA      780
CTTTCCTTTT AAATGCGTAT ACTGCACCTG CAACGGCAGC GACAGTTCCT GCGACACCTG      840
TTACAAGACC TTTAGCGAAT CCTTTAGCCA TGAGTCTTCC TCCTTTATAT TCTCAATCAG      900
CCAGCCTCCT CAAGAGGTCA CATTTTCTG ACTGACCTTT TTGTGTTATA ATAATAGTAA      960
CGAAAAAATG GGAATTTTTC AAGGAAAAAA GATGAGAACA AAA                      1003

```

## (2) INFORMATION FOR SEQ ID NO: 346:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 750 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

```

CCGCACGTAC TATTCCAGAT GCCGAGGAAG TGGACCTCAT CCTCGTTGGC GCAACTGGTC      60

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1365

TCAACGCCTT TGAACGCCTC TTGGTCGGCT CTTTCATCTGA ATACATACTC CGCCATGCTA	120
AGGTCGATTT GCTGGTTGTG AGAGAACAAG AAAAAACCTT ATAATCACAA AGAAAAGGAG	180
CCCCTAGCTC CTTTTTGTTC ACGATTATT TCTCTCTTA TGGCGTTCGT AAGCCTTGAG	240
CTGGCGCTGC AGTTCCTTTT TAATAGCAGG TTCTGGAGCA TATTTTCTT CCCAATTATC	300
TGGTTTAAAG ATTTTATGGG TCACTGGATC AAAATGAGCC TTGCCATCTG GAAAAATTTT	360
CCCCATATTG GCCTGATGGA CAATATCAAA AATACGTTCT GGGTCCACCC CCATCAAGAC	420
AAAAGTCCCG TAGGTGAAGT AAAGCGTGTC AATCAAGGCA TCCACTTGCC CTATCAAATC	480
TTGCTGAGCA GGTGTCTTCT TGGCTACTTT ATCTGCTGCC TTATCAAGGG CCTGATGAAG	540
TTGCGATACA GCTTGACCAA AATCTTCTTC AGAAGGACTG GCTGCTCGAA CAAACTCCAC	600
CAATCTTCT ATTTTAAAC CAGCCCTATG GGTGCACCC TCTAAATCCC AAGCTCGAGG	660
TTCTTCTGG GTTCGTTTAT CCATCATGTG GTGAAAGTC TTGACCTTAT TGAAATGATA	720
GTACCGGCTG ACAAGACTT TTTCTGAAGA	750

(2) INFORMATION FOR SEQ ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 596 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

CGCAACATAC GGATAACCTC CAAAGAATAT TTTTATATTA TAGCAAAGCT TTAAATTGAA	60
TGTTAGAGTC TTGTTCAAAA CAATCATCAA AACCACGTGG ATGATGGTAT TCTACTAAGT	120
GTTGATCTTG AGGATAAGTG TACTTACCGC CAACTTCCCA GATAAATGGA TGGAAATCGT	180
ATTGCAAGCG ATCTTTTCGC ATTTTCCAAA GTTCTAGAAT CTCATTAGTA GAAGCCATGA	240
AGTTAGACCA GATATCATAG TGAAGTGGG TAATGACTTT GGTACGCAGA TTTTCTGCCA	300
TACGAAGAAG GTCGATAGAT GTCATTTTGT CTGGGATACC TACCGGATTT TCACCATAGT	360
TATTCAAAGC AACATCAATT TTAAAGTCTT TACCATGTTT TGCAAAATAG TTTGAGAAGT	420
GAGAATCTGC ACCATGATAG ATGGTTCCAC CTGGTGTTTC AAAGATATAG TTAACAGCCT	480
TTTGAGCCAT TTCTTCATCT GTAACAGCCA AGCCAGCagT TCACCGCCTG TCTCATCAGC	540
ACCGTTCACT GGGAGAGTTA CCAAGCAAGT ACGGTCAAAT GATTCTACTG CATGAA	596

(2) INFORMATION FOR SEQ ID NO: 348:



1366

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 673 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

CAGAGTCAAC AGCCTGAGTT GAAGGCAACT TTAGACACAG CAGTTACGAC AGCTGAATGA	60
GCTCCTCCAT CAGTTTTTTC TTTAATGAGT CCAGCTACAT CTTCAACTTC GAGGCCGTTA	120
ATCACAATGT CAGCGCCTAC TTCTTTTGCA AGGGCAAGTT TGTCAATTGTT GATATCGACT	180
GCGATAACAT GAGCATTGAA TACTTTTTTA GCGTATTGAA CAGCGAGGTT ACCAAGTCCA	240
CCAGCACCGT AAAGAACAAC CCATTGGCCT GGTCAACTT TTGCTTCTTT GATAGCTTTA	300
TAGGTTGTTA CTCCAGCACA TGTGATAGAA GAAGCTTGGG CTGGATCAAG TCCGTCAGGA	360
ACTTTGACAG CATAGTCAGC AGTTACGATA CATTGTTGAG CCATACCACC GTCTACTGAG	420
TAGCCAGCAT TTTTCACTGT ACGGCAAAGG GTTTCGCGAC CAGTTGTACA GTATTGCGAA	480
GTGCCACATC CTTCAAAGAA CCAAGCAACG CTGACGCGGT CACCGACTTT AAGGCTTTTC	540
ACATCTGGAG CAATCTCTTT AACGATACCG ATACCTTCGT GCCCAAGAAC ACGTCCTGGG	600
ACTTGACCAA AGTCACCATG AGCAACGTGG AGGTCGGTGT GGCAAACGCC CACAGTATTC	660
ACTTCTACAA GTG	673

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GTACCCTACA AATGCTTTAC AGTATGGGTT GAGGGTGGTC AATGGAACTA TGGAGTAGGT	60
TGGACAGGAA CTTTGGGATA TTCTGATTAC TTACATTCTA CTCGATATCA TACAGCAACT	120
GTTAGACATG GGGGTAGAAC CTCTAAGGAT TATGCAAAAC CTGAGGCATG GGCTAGAGCT	180
TCCCTCACCA AGATTCCG	198

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 891 base pairs  
(B) TYPE: nucleic acid

1367

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

```

GCTTCTTCTA TAGACAAAAA TATCATGGGT AAAATAATCA AGGCTATAGC TAGAAGGAGG      60
GACCAATCCA CTACTAATCC TAAGAACAAA ACACTCAAGA GAGCAGAAGA GAGAGGTTCA      120
CTGGCACTGA TAACGGCAAC CACCAAAGGA GAAACCAAGG ACACAGCCTT CATGGAAATG      180
AAAAAAGCAA AAGCCGTTCC AAAGAAAGCG ATAATGAGGC AAATCAAGAT ACTCCAAATA      240
TCAAGAGTAA AGGAAAGCTG ATAAACCGGC GAGAGGACAT TGCTAAACAA ACCTGCCAAA      300
ATCATCCCCC ACCCAACCGT AGGAACAAAA CCATAACGCT TAGCAAAAGG TTGGGGCAAG      360
ATAACATTAA ACATAACACC CATGGCACTC AGCAAACCTG TTATAAGAGC TAGCGGCGTC      420
ATGGATAACT GAGAGAGGTC TCCCTTTGTC GCCATCAAGC AAACACCCAG CATGGCAACC      480
AAAACATAGA AAACAGCGCT TTTTGACGCT CGTTTTTGAT AAACCAAGCG ATTGTAAAAG      540
AGGATAAAGA CAGGGCTAAT AAAGTGTAAA ATAGTTGCTG TCGTAGCATT TGAGTATTCT      600
ACACAGAGAT AGAAAAAATA CTGAACGTAA AAAATCCCCA AAATAGCATA GGCTAAAAAG      660
GCGAGGTAAT TTTTCTTGTC TCGCCAAATA TCTAGCACTT GCGATTTTAA TTGTATTGCA      720
GACCAAAATGA GTACAAGACT CCCTGCCAGT GTCAAACGCA TAGAGGTAAT CCAGCCCGAA      780
GACACCTGAT AATGAGTAAA GAAGTACTCT CCTAAAATTC CACAGATTCC CCATATTAAG      840
CCGGATAGGA GCGAATAAAT TTTTCCGTGA ACAATCTTTT TCTGATACTG A              891

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(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

```

GAAAGCGTTC AATAGAACAT TGCTTTTTTA TTTTtagAGT AAGCTAAGCG CTTcAGCATC      60
TGCGATGATG GTTACATCAG GGTGATTTTG GAGGCTACTT GCAGGTAGGT TCTCAGTCAC      120
TGGGCCAGAT ACTGTTCCGG CAATGGCTTC TGCTTTCGAC TCACCGTAAG CAAAAAGAAT      180
AATAGACTTG GCATCCAAAA TGTTTTTAAT CCCCATTGAA ATAGCTTGGG TTGGGACGTC      240
TTCAATCTTG GCAAAGAAGC GTGCATTGGC TTCGATAGTA GACTGGTCAA GTTCTACTAG      300

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ATGCGTTTGA CTGTCAAATG GAGTG 1368 325

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

CAAGAGCAGT TTGATGATTT TTGATAAGCA TGCGAATTTA AAATACAAAT ATGGCAATCG	60
CAAGTTTTCG TGTAGAGGCT ATTATGTAGA TACGGTAGGC CGTAATCAGA AAGTGATAGC	120
TCAATATATT CAGAATCAAT TACAAGAAGA CAGAGTAGCA GACCTAGCTC ACGTTATTCC	180
AGTCAGTAGA TCCGTTTACT GGCGAAATAA ATAAGAGGAA GTAACGThAA GTGCTTTAGC	240
ACCTGCTCGG GAAAGTGGTG CGCGAGGAAG CTATTTTCAGG ATGCTTTGGC CCTGGCCGGT	300
AGAAGCGTTA TAGCCGAGA CTACGACACT TCACACTGGT GGT	344

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 692 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CCCTATCCCT GCTATTGGGG CTGCTCTCAT TGCTGCTTTG GCACAAATCA GTCTTCCAAT	60
TGGACCTGTT CCCTTCACTC TGCAAACTT TGCAATCGGC TTGATTCTAC TGTCTTTAGA	120
CCGAGAGAGG CTGTAATTTG TGCTGGACTC TATCTTCTTC TAGGTGCTAT CCGTCTTCCT	180
GTCTTTGCAG GAGGTGGAGC TGGTTTTCAG GCTTTAGTTG GCCCTACTGC AGGCTATCTT	240
TGGTTTTATC TCGTTTACTC TGGACTTACT TCCTCTCTAA CCAACAGCAA GAGTGGTGT	300
GTTAAGATTT TTCTTGCAA CCTCTTGGGT GATGCCCTTG TCTTTGTCGG CGGGATTCTC	360
AGCTTGCAAT TCCTAGCTGG AATGGCATTT GAAAAAGCTC TTGCTGTGGG GGTCTCTCCC	420
TTTATCATTC CAGACCTTGG CAAACTTCTA GCTATTAGTT TTATTAGCCG TCCCCTACTT	480
CAACGCCTTA AAAATCAGGC TTACTTTACT AACTAAAAA GGATATCGAG TTATCATGAC	540
TCAATATCC TTTCTTTTAT TTTGAAAACT TATACTCAAT GAAAAACAAA GAGCAAACTA	600
GGAGCTAGC CGCAGGCTnG CAAACACTG TTTTGAGGTT GTGGATGAAA CTGACGAGTA	660

1369

AnATCTCATA CATACGGCAA GGCAAAGCTG AC

692

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1005 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GTGATGGACT ACTGGTCAA AACGCATCCA GAAGATTTT TCGATAATGT CGGACCTCTT	60
GTAGCCAGTA ACTTTTTTCA TACTTACACC GAAGATTTC ACTTGATGAA GGAAATTGGA	120
GTTAATTCTT TCCGCATTC CATCCAATGG AGTCGACTCA TCAAGAATTT AGAGACAGGT	180
GAGCCTGATC CAAAAGGTAT TGCTTTCTAC AATGCCATCA TTGAAGAAGC TAAAAAGAAC	240
CAGATGGATC TTGTGATGAA TTTACATCAT TTTGATTIAC CAGTGGAAC TCTTCAAAAA	300
TACGGTGGTT GGGAAAGCAA ACATGTAGTG GAGTTATTCG TGAAGTTTGC CAAGACTGCT	360
TTCACATGCT TTGGAGATAA GGTTCATTAC TGGACAACCT TCAATGAGCC AATGGTCATT	420
CCAGAAGCAG GGTACTTATA TGCTTTCCAT TATCCAAATC TAAAGGAAA GGGAAAAGAG	480
GCCGTACAAG TCATCTATA TCTAAACCTT GCTAGTGCAA AAGTGATTCA ACTATATCGC	540
TCATTAGAAC TTGATGAAA GATTGGGATT ATTTTAAACT TGACACCTGC TTATCCAAGA	600
AGTAATTCTC CAGAAGACTT AGAAGCAAGT CGATTTACAG ATGACTTCTT TAACAAAGTC	660
TTCTTGAATC CAGCTGTAA AGGAACCTTC CCAGAAAGAT TGGTAAAACA GCTAGAGAGA	720
GATGGCGTGT TATGGAGTCA TACCGAAAA GAGCTTCAAC TGATGAAATC AAATACGGTT	780
GATTTTCTTG GAGTAACTA CTACCATCCA AACGTGTTT AAGCACAAGC AAATCCTGAG	840
GAATATCAGA CGCCCTGGAT GCCAGACCAA TACTTCAAAG AGTATGAATG GCTGGAGCGT	900
CGCATGAATC CATATCGTGG TTGGGAAATT TTTCCGAAAG CCATTTATGA TATTGCTATG	960
ATTGTGAAGG AAGAATATGG TAATATCCCA TGGTTTATCA GTGAA	1005

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 973 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CCGACAAGCA ATATTAAAAA GAGTAAACTA TTAAGTAGTT AATTAACCGG TTTATTACTT	60
TATAGTGAAT CAAATATACT TAAGAAAACA GGAAAGAATG AAAATTAATA AAAAATATCT	120
AGCAGGTTCA GTGGCAGTCC TTGCCCTAAG TGTTTGTTCC TATGAGCTTG GACGTTACCA	180
AGCTGGTCAG GATAAGAAAG AGTCTAATCG AGTTGCTTAT ATAGATGGTG ATCAGGCTGG	240
TCAAAGGCA GAAAACTTGA CACCAGATGA AGTCAGTAAG AGGGAGGGGA TCAACGCCGA	300
ACAAATTGTT ATCAAGATTA CGGATCAAGG TTATGTGACC TCTCATGGAG ACCATTATCA	360
TTACTATAAT GGCAAGCTTC CTTATGATGC CATCATCAGT GAAGAGCTCC TCATGAAAGA	420
TCCGAATTAT CAGTTGAAGG ATTCAGACAT TGTCAATGAA ATCAAGGGTG GTTATGTCAT	480
TAAGGTAAAC GGTAATACT ATGTTTACCT TAAGGATGCA GCTCATGCCG ATAATATTCG	540
GACAAAAGAA GAGATTAAAC GTCAGAAGCA GGAACGCAGT CATAATCATA ACTCAAGAGC	600
AGATAATGCT GTTGCTGCAG CCAGAGCCCA AGGACGTTAT ACAACGGATG ATGGGTATAT	660
CTTCAATGCA TCTGATATCA TTGAGGACAC GGGTGATGCT TATATCGTTC CTCACGGCGA	720
CCATTACCAT TACATTCCTA AGAATGAGTT ATCAGCTAGC GAGTTAGCTG CTGCAGAAGC	780
CTATTGGAAT GGAAGCAGG GATCTCGTCC TTCTTCAAGT TCTAGTTATA ATGCAAAATCC	840
AGCTCAACCA AGATTGTCAG AGAACCACAA TCTGACTGTC ACTCCAACCT ATCATCAAAA	900
TCAAGGGGGA AACATTTCAA GCCTTTTACG TGAATTGTAT GCTAACCCCTT ATCAGAACGC	960
CATGTGGGAT CTG	973

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 843 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GGTCGCATCT GCAATATCTG TCGCCTCCAC ATAAGCGACA CCAGCCTTGT CTGCTGCCCC	60
TTTGACACGT TCTGCAGATT GACCCAGGAT GACCATCTTC TTGAGTCCAG TAATGTCTGG	120
CACCAATTCG TCAAATCAT TGCCACGGTC CAAACCACCT GCAATCAAGA CGACCTTGCT	180
GTGTGCAAAT CCTGACAAGC TTTTGTAGTA GCCAAGATAT TAGTTGATTT ACTGTCGTTA	240
TAGAATTTAA CACsCTTGAT GTCATCCACA AACTGGAGAC GGTGTTTGAC ACCACCGAAG	300
GCTGAAAGAG TTTCTTGAT GGTGTTGATTG TCCACATCAC GAAGCTTGGC TACAGCAATA	360

1371

GTCGCAAGGG CATTTCAC ATTGTGGCTA CCTGGAACAC CGATTTCATT CGCTGCCATG	420
ACTACTTCAC CACGGAAGTA GAGTTGACCA TCTTCCAGAT AAGCTCCATC AACCTTTTCA	480
AGTGTTGAAA ATGGTACAAC AGTGGCTTCT GTCTTGGAAG TCAAGTCTTT TGCCAAGTCT	540
TGATTAAAGT TCAAGACAAG GAAATCAGCT GCTGTCATCT TGTTCCTGGAT ATTCCACTTG	600
GCTGCTACAT ATTCCGAAAA TGACCCATGG TAGTCGATAT GAGTTGGCAT GAGGTTGGTA	660
ATAACCGCAA TCTCTGGATG GAATTCCTGA ACACCCATGA GTTGGAAGA AGAAAGTTCC	720
ATAACAAGCG TGTCTTATC TGATGCTATT TGAGCAACCT GACTAGCTGG ATAGCCGATA	780
TTCCCTGATA AAAGACCATG TTGGCCAGCA GCAGTCAAAA CTTCCCGGGn TCCTCTAGAG	840
TCG	843

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 807 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

TTTTTTTAT ATTTTTTTTA TTTATTATTT TTTGGCAAAA AAGACCAATT TGCTTTGGAG	60
CATTGCTTCT GCATTAAATT GTCTATTTT GCTCGTCTG TTACGCTCTT TGTATCATGT	120
ATTAACTAGC AAGTGCAACT TGCAAACTAC TAGTAAGAGG AGAAAAACAA AATGGTTATG	180
ACTGACCCAA TCGCAGACTT CCTAACTCGT ATTCGTAATG CTAACCAAGC TAAACACGAA	240
GTAATTGAAG TACCTGCATC AAACATCAAA AAAGGGATTG CTGAAATCCT TAAACGCGAA	300
GGTTTTGTAA AAAACGTTGA AATCATTGAA GATGACAAAC AAGGCGTCAT CCGTGTATTT	360
CTTAAATACG GACCAAATGG TGAGAAAGTT ATCACTAACT TGAAACGTGT TTCTAAACCA	420
GGACTTCGTG TCTACAAAAA ACGTGAAGAC CTTCCAAAAG TTCTTAACGG ACTTGAATTT	480
GCCATCCTTT CAACTTCTGA AGGTTTGCTT ACTGATAAAG AAGCACGCCA AAAGAATGTT	540
GGTGGTGAGG TTATCGCTTA CGTTTGGTAA AATCAAGATA CAAAGCTCGT AAAGAACAAA	600
GCAAAATTAG GAAGTTGGAG AAGTTTGT TTACAAACAGGC CAACTTATCT ATTTTGCACA	660
GTTCTTAGAG CGTGTTCACT TCAGCTCTTG AGCTAAGTAA CTATCTGAAC CCCGTGAAAA	720
CTGCCCCTGC TGGCATGTTC GGGTAACAGG AGAaAATAAA CATGTCACGT ATTGGTAATA	780
AGTTCAGCTA AGGCCTTCGT AAAAGTT	807

1372

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 653 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

CCCAGTATTT TTGTCCAAGC ACGACCAGAA AAGGATGATA CAGATCTGGA ATGGGCTCTC	60
TTAACCATCT tTGAACAAAA TCCTCAGGCT CAGGTCAC TA TTTTCGGTGC CTGGGTGGC	120
CGTATTGACC ATATGTTGGC CAATGTCTTT CTGCCTAGCA ATCCTAAGTT GGCACCTAT	180
ATGCATCAAA TAGAAATTGA GGATGGGCAA AACTTGATTA CTTATTGTCC AGAAGGAATC	240
AGTCAGCTAG AACCTCGTTC AGACTACGAC TATCTAGCCT TTATGCCAGT TCGGGATAGC	300
CAAGTATGAG TTGACAGAGG AAAATTTTTT CTTAAAAAAA CTGTACGCTT CTAACGAATA	360
TATAGATAGG GAAGTGTCGG TAACTTGCCC AGATGGTTAT GTGGTCGTAC TGCATAGCAA	420
GGACAGGAGG TAGGATGGAA AGTTTACTTA TTCTATTATT AATGCCAAT CTAGCTGGTC	480
TCTTCTGAT TTGGCAAAGG CAGGATAGGC AGGAGAAACA CTTAAGTAAG AGCTTGGAGG	540
ATCAGGCAGA TCATTTGTCA GACCAGCTGG ATTACCGCTT TGACCAAGCC AGACAAGCCA	600
GCCAGTTAGA CAAAAAGAT TTGGAAGTGG TTGTCAGCGA CCGTTTGCAA GAA	653

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 641 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CACCATGTGA TGTGACGCTG GCCACAGCTG TCAGAAATCT GGCAGCCAT CGTGTGCAAT	60
GACTCTTCCC GATGTAATCT TGTTTCATAGT CCTTTGATGA ATATGTTCAA GCTGTAGAAG	120
GTGCGCTTCC TGAACACTTA TCAACTGTTA CAGCGAGTT GACCAGTCAG GAAACAGATG	180
GCTGGTACAC ACTTGCCAAC ACTTCTTCAT CCCGCATTTA CCTAAAACAA GCCTTCCAAG	240
AAAATAGCAA CCTCCTAGAG CAAGTGGTAG AACCTTGAC TATTATCACT GGTGGACACA	300
ACCACAAGGA CCAGTTGACC TATGCTTGGG AACACTTTT GCAGAATGCG CCACATGATA	360
GTATCTGTGG CTGTAGCGTG GACGAAGTTC ACCGCGAGAT GGAAACGCGT TTTGCCAAGG	420

1373

TCAACCAAGT AGGAAACTTT GTTAAAAGTA ACTTGCTCAA CGAGTGGAAG GGTAAAATTG	480
CTACGGATAA GCCTCAAAGT GACTATCTCT TTACTGTCAT TAACACAGGC TTGCATGATA	540
AGGTCGATAC TGTCAGCACA GTGATTGATG TGGCGACTTG TGATTTCAAG GAATTGCACC	600
CAACAGAAGG CTACAAAAAG ATGGCTGCTC TTATCTTGCC G	641

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1958 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CCTCAAGGCC AATTGAAGG CTCTAAAACA ATGGAAGAGT GCTACACAGA TGTGACAGAA	60
TTTGCCATTC CAGCAAGTAC TCAAAAGCTT TACTTATCAC CAGTTT TAGA TGGCTTTAAT	120
AGCGAAATTA TTGCTTTTAA TCTTTCGACT TCACCCAACT TAGAACAAGT ACAAACAATG	180
TTAGAACAGG CATTCAAAGA GAAGCACTAC GAGAATACGA TTCTCCATAG TGACCAAGGC	240
TGGCAATATC AACACGATTC TTATCATCGG TTCCTAGAGA GTAAGGGAAT TCAAGCATCT	300
ATGTCACGCA AGGGCAACAG CCAAGACAAC GGTATGATGG AATCTTTCTT TGGCATTTTA	360
AAATCCGAAA TGTTTTATGG CTATGAGAAA ACATTTAAAT CACTTAACCA ATTGGAACAA	420
GCCATTATAG ACTATATTGA TTAATAACAAC AACAAACGAA TTAAGGTAAA ACTAAAAGGA	480
CTTAGTCCTG TGCAGTACAG AACTAAATCC TTTGGATAAA TTAATTGTCT AACTTTTGG	540
GGTCAGTACA AACTCTTGC TACTATGCGT TTTATTATTG AAAGACTTAT TGGACTTTCT	600
CTCAAATCGA GTTTTACTC AATTTTCTTA CTGATTGGG ATTGAAATTC CAATTAATTT	660
CTCTGAGTAG AGTGTCTTGA TATTGGCTTC ATCAACAGAG GCCTTATCAA TTTTACGTTT	720
CAAGAAAAAT TCTTGAATGG TTTGATTTT AGGCTCACGA ATAGCACGGT GTTTGTTTGA	780
GATGAGGATT TCATAGTGAA GCGGAGCTTG GGTAAAAATA ACATCTGTAT TCCCTGCAGA	840
ATAAACCTCA ACAAGGGTTG CATCGGTACT TTCTAGCTGA CTTTTTACAA GTTGCGAGTG	900
TGAGTTTGTG GTATTGATAA GCTTCATAAT ATTTCTCCG ATTTTCTAAT TCTATTATAG	960
CACTTTTGA ATAAAGTCGC TTGATTTATA CTCAATGAAA ATCAAAGAGC AACTTAGGAA	1020
GCTAGCCGCA GGCTATACTT GAGTACGGTA AGGCGACGCT GACGTGGTTT GAATTTTATT	1080
TTCGAAGAGT ATTAGCCAAT CTTATGCTGT TTTTCCAAG ATTCAATGGC CCATTTATGG	1140



1374

CTACCACGTT TAAGGTTTTT GATAGCCTCG TCAATAGGGA ACCAGGCAAT ATGATTAAAG	1200
TTTCTCTAGTG GCTTTTGTTAC TTCTTTTGAAA GGAGTTGCTT CATAGAGGTA GGCAGGATTG	1260
TAGTAGTAGG TATCACGATG ACGAGAATAG AAATATTTCGT CAGCTTGTCG GTAATAGGTA	1320
CCAATTTCTG CTGTGAAACC AAGCTCTTCA ATCAACTCAT GCTTTAGGGC TTCCTGATGA	1380
TTTTCACCTG CTTCAATTTC TCCACATGGT AGGAACCAAG CACCATTTCG TTCTTGAACA	1440
AGAACAATTT GTTTTGTTC AGGATTAGGG ATAAGTGCAT ATACGCCATA GCGAGCAATA	1500
TAGTCTGTAT TCACTTTTTT TCTCCGAAAG TTGGGTTTGC CATTGCATTT TCCTCATTAT	1560
CTAGTATCGT TATTATTATA GTGAAATGAA CAAAAAATAG TACACAATGT GGTATAATCT	1620
TCTTATGGCA TATTCAATAG ATTTTCGTAA AAAAGTCTC TCTTATTGTG AGCGAACAGG	1680
TAGTATAACA GAAGCATCAC ACGTTTCCA AATCTCACGT AATACCATT ATGGCTGGTT	1740
AAAGCTAAAA GAGAAAACAG GAGAGCTAAA CCACCAAGTA AAAGGAATAA AACCAAGAAA	1800
GGTTGATAGA GATAGACTTA AAAACTATCT TACTGACAAT CCAGACGCTT ATTTGACTGA	1860
AATAGCTTCT GAATTGGCT GTCATCCAAC TACCATCCAC TATGCGCTCA AAGCTATGGG	1920
tACACTCGAA AAAAAAAGA ACTACACCTA CTATGAAC	1958

## (2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 851 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

TATGAAATTA AGTTATGATG ATAAAGTTCA GATCTATGAA CTTAGAAAAC AAGGATATAG	60
CTTAGAGAAG CTTTCAAATA AATTGGGAT AmACAATTCT AATCTTAGGT ATATGATTAA	120
ATTGATTGAT CGTTACGGAA TAGAGTTCGT CAAAAAAGGA AAAAATCGTT ACTATTCTCC	180
TGATTTAAAA CAAGAAATGA TTAATAAAGT CTGACATGAA GGCTGGACTA AAGATAGAGT	240
TTCTCTTGAA TACGGTCTCC CAAGTCGTAC GATACTTCTT AACTGGCTAG CACAATACAG	300
GAAAAACGGG TATACTATTG TTGAGAAACC AAGAGGGAGA GTACCTGAGA GCGGAGAATG	360
CCATCCTAAA AAAGTTAAGA GAACTCCGAT TGAAGGAGGA AAAAGAGAAA GAAGAAAGAC	420
AGAAATTGTT TAAGAATTAA TGACTGAGTT TTCGTTAGAT CTTCTTTTAA AAGTCATTAA	480
ACTAGCTCGT TCGACCTACT ACTATCACCT GAAACAGCTA GATAAACCAG ATAAGGACCA	540
AGAGCTTAAA GCTGAAATTC AATCCATTTT TATCGAACAC AAAGGAAATT ATGCTTATCG	600

1375

TCGGATTTAT TTAGAACTAA GAAATCGTGG TTATCTGGTA AATCATAAAA GAGTTCAAGG	660
CTTGATGAAA GTACTCAATt TACAAGCTAA AACGCGACAG AAACGAAAAT ATTCTTCTCA	720
TAAAGGAGAC GTTGGCAAGA AGGCAGAGAA TCTCATTCAA GGCCAATTTG AAGGCTCTAA	780
AACAATGGAA CAGTGCTACA CAGATGTGAC AGAATTTGCC ATTCCAGTAA GTACTTAAAA	840
GCTTTACTTA T	851

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1168 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

GGGTAGAATC GATATCTCCA ATGAGTTGGT tTAGCTGGTG AAACGTGAAA AAGATTTCGw	60
CCAATTCAAG GTTGAGGCAT CGCAAATAT GGACTGTTTC CTCGTCAGTT CTGGAAAGAA	120
AACGGGATAA GGTTCGCTGT GAAGCAAGCT GCCCTCCTTC CAACAATTTT GGAAAGTAGG	180
CATCAGCTGA CAATCTTTA CAAGCATAGT CCGTTCCTTA ACCTGTTAAC AGTTGAAAGA	240
GGAAGTGGAC AAGGATATCT GAATCCGAAT AACGACAGTA GCGGCGTTGG TCATTCGTTA	300
CTAAATACTT AGAAATCCGC TCTTTTAGTT TCAACTGGGA AAAAAGTTCC TGA AAAAAGA	360
TAAGACCACC ATACTGGGTT AAATGACCTC CATCGAAAGA TAGTTGGTAA AAAGACTTGT	420
TTTGGAAGTG ATGATTGGT AAACGTTC A TGAGATTTC CTTTCTTTT GTGTTTTTTT	480
CTACACTTAT ACCATAAAGG GGAAACTCTT TTTGTCTAG TAAAAACAC CCATTGGGTG	540
AAAAAGAAA CCATCCAGGA TCTAAGCTAA GGCAAGGATT CTGGATGGTT TTTAGATTG	600
GGTGAATAA TTGGGGTTT AGCTGCTTGC GGCCAATCAG GTTCAGATAC AAAAATTAC	660
TCATCAACCT TTAGTGGA TCCAATACA TTAACTATC TATTAGACTA TTACGCTGAT	720
AATATAGTCA ATTGAAACAA GAACAAGACA AAAGAGCCTC ATAAAAGGTA TTGCAACTTG	780
GTAATACCTT TTTGAGGTGC TTTTTCATAT GAGCCCATGT TTTCTCAATA GGATTGTACT	840
CAGGTGAGTA GGGAGGAAGA GGTAAAAGTT TATACCCAAA CTCTTCACAC AAGAGTTCTA	900
ACTTACCCAT TCTATGGAAT CTTGCATTAT CCATAATAAT AACCGATGGT GTGTTTAATG	960
TTGGTAAGAG AAATTTCTGA AACCAAGCTT CAAAAAGTC GTCGTCATC GTCTCTTCGT	1020
AAGTTATTGG AGCGATTAAC TCACCATTG TTAGACCTGC AACCAAAGAA ATCCTCTGAT	1080

1376

ATCTTCTTCC AGATACTTTG CCTCTTCTTA ACTGACCTTT TAATGAGCGA CCATATTCTC 1140  
 GATAAAAATA AGTATCGAAT CCTGTTTC 1168

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4483 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GTCAGCTTCA GCAAGCCCAT CAGCTTCTGA ATCTGCATCA ACCAGTGGCT CCGCTTCAGC 60  
 GTCAACCAGT GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC 120  
 GTCGGCCTCA GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCGGC 180  
 TTCAGCAAGC ACAAGTGGCT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC 240  
 GAGTGGCTCT GAGTCAGCAT CAACGAGTAC GTCAGCCTCA GCAAGCACAT CAGCTTCTGA 300  
 ATCTGCATCA ACCAGTGGCT CAGCCTCAGC ATCGACAAGC GCCTCAGCTT CAGCAAGTAC 360  
 CAGTGGCTTCA GCCTCAGCGT CGACAAGTGC GTCGGCCTCA ACCAGTGCAT CTGAATCGGC 420  
 ATCAACCACT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC 480  
 ATCGGCTTCA GCATCAACCA GTGCCTCGGC TTCAGCGTCA ACCAGTGGCT CAGCTTCAGC 540  
 AAGTACCAGT GCTTCAGTCT CAGCATCAAC AAGTGCTTCA GCCTCAGCAT CGACAAGTGC 600  
 CTCGGCTTCA GCAAGCACAT CAGCATCTGA ATCAGCGTCG ACAAGCGCCT CAGCTTCAGC 660  
 AAGTACCAGT GCGTCAGCCT CAGCGTCGAC AAGTGCGTCA GCCTCAGCAA GTACTAGTGC 720  
 ATCAGCTTCA GCATCAACGA GTGCATCGGC TTCGGCGTCA ACCAGTGCAT CAGAGTCAGC 780  
 AAGTACCAGT GCGTCAGCTT CCGCATCAAC AAGTGCTTCG GCTTCAGCAA GCACCAGTGC 840  
 GTCGGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCCTCA ACCAGTGGCT CAGCCTCAGC 900  
 AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGGCTCC GCTTCAGCAA GTACTAGCGC 960  
 CTCAGCCTCA GCGTCAACAA GTGCATCGGC TTCAGCGTCA ACGAGTGGCT CTGAATCGGC 1020  
 ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC 1080  
 ATCGGCTTCA GCATCAACGA GTGCGTCCGC TTCAGCAAGT ACTAGCGCCT CAGCCTCAGC 1140  
 GTCAACAAGT GCATCGGCTT CAGCGTCAAC GAGTGGCTCT GAGTCAGCAT CAACGAGTGC 1200  
 GTCAGCCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGGCT CAGCCTCAGC 1260  
 ATCGACAAGC GCCTCAGCTT CAGCAAGTAC CAGTGGCTCA GCTCAGCGTC GACAAGTGCs 1320

1377

TCrGCTTCAG CAAGTACCAG TGCCTCAGCC TCAGCAAGTA CCAGTGCKTC AGCCTCAGCG	1380
TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG CATCAACCAG TGCCTCAGCC	1440
TCAGCAAGTA CTAGCGCCTC AGCCTCAGCA TCAACGAGTG CGTCCGCTTC AGCAAGTACT	1500
AGTGTCATCAG CTTCAGCAAG TACTAGCGCC TCAGCCTCAG CGTCGACAAG CGCCTCAGCT	1560
TCAGCAAGTA CCAGTGCGTC AGCCTCAGCG TCGACAAGTG CGTCGGCTTC AGCAAGTACC	1620
TCAGCGTCTG AATCAGCATC AACAAAGTGG TCGGCTTCAG CATCAACGAG TGCATCAGCT	1680
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	1740
AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCCG CATCAACAAG TGCCTCGGCT	1800
TCAGCAAGCA CCAGTGCTTC GGCTTCAGCG TCAACGAGTG CGTCTGAGTC AGCATCAACG	1860
AGTGCGTCAC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCACTTC	1920
CGCATCAACA AGCGCCTCGG CCTCAGCAAG TACAAGTGCT TCAGCCTCAG CATCAACCAG	1980
TGCATCAGCT TCAGCCTCAA CAAGTGCTTC AGCCTCAGCG TCAACCAGTG CCTCGGCTTC	2040
AGCAAGTACC AGTGCGTCAG cTTCAGCAAG CACAAGTGGC TCAGCTTCAG CATCAACCAG	2100
TGCTTCGGCT TCGGCATCAA CAAGTGCTTC AGCATCAGCA TCAACGAGTG CGTCA <sub>s</sub> CTCA	2160
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACCAGTGCAT CAGCCTCAGC AAGTATCTCA	2220
GCGTCTGAAT CGGCATCAAC GAGTGATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA	2280
GCGTCAACCA GTGCATCAGT CTCAGCAAGC ACCAGTGGCT CGGCTTCAGC ATCAACCAGT	2340
GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT CAACGAGTGC GTCAG <sub>c</sub> CTCA	2400
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACGAGTGCAT CGGCTTCAGC AAGTACCAGC	2460
GCCTCAGCTT CAGCAAGCAC CAGTGCGTCA GCCTCAGCAA GTACCAGCGC CTCAGCCTCA	2520
GCAAGCACCA GTGCCTCAGC TTCAGCAAGT ACCAGTGGCT CAGCCTCAGC GTCGACAAGT	2580
GCGTCGGCTT CAGCAAGTAC CTCAGCGTCT GAATCAGCAT CAACGAGTGC ATCAGCTTCA	2640
GCATCAACAA GTGCTTCAGC TTCAGCAAGT ACCAGTGGCT CGGCTTCAGC ATCAACGAGT	2700
GCTTCAGTCT CAGCGTCAAC CAGTGCTCT GAATCAGCAT CAACAAGTGC CTCGGCTTCA	2760
GCAAGCACCA GTGCGTCGGC TTCAGCAAGT ACTAGTGCAT CGGCTTCAGC ATCGACAAGT	2820
GCGTCTGAAT CGGCATCAAC GAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCAGCCTCA	2880
GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGGCT CCGCTTCAGC GTCAACCAGT	2940
GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCGGCCTCA	3000
GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCCGC TTCAGCAAGC	3060

1378

ACAAGTGCGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCGTCG	3120
GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCCGCCT CAACCAGTGC GTCGGCTTCA	3180
GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT	3240
GCGTCTGAGT CAGCATCAAC GAGTACGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCG	3300
GCATCAACCA GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT	3360
GCTTCAGCCT CAGCGTCGAC AAGTGCGTCG GCCTCAACCA GTGCATCTGA ATCGGCATCA	3420
ACCAGTGCGT CAGCCTCAGC AAGTACTAGT GCATCAGCTT CAGCATCAAC GAGTGCATCG	3480
GCTTCAGCAT CAACCAGTGC CTCGGCTTCA GCGTCAACCA GTGCGTCAGC TTCAGCAAGT	3540
ACCAGTGCTT CAGTCTCAGC ATCAACAAGT GCTTCAGCCT CAGCATCGAC AAGTGCCTCG	3600
GCTTCAGCAA GCACATCAGC ATCTGAATCA GCGTCGACAA GCGCCTCAGC TTCAGCAAGT	3660
ACCAGTGCGT CAGCCTCAGC GTCGACAAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA	3720
GCTTCAGCAT CAACGAGTGC ATCGGCTTCG GCGTCAACCA GTGCATCAGA GTCAGCAAGT	3780
ACCAGTGCGT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT CAGCAAGCAC CAGTGCGTCG	3840
GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA GTGCGTCAGC CTCAGCAAGT	3900
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA	3960
GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA GTGCGTCTGA ATCGGCATCA	4020
ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT CAGCGTCAAC AAGTGCATCG	4080
GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCGTCA	4140
ACAAAGTGAT CGGGTTCAGC GTCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTGCGTCA	4200
CTCTCAkCAAG CACATCAGCT TCTGAATCTG CATCAACCAG TGGCTCACTT CCGCATCAAC	4260
AAGCGCCTCG GCCTCAGCAA GTACAAGTGC TTCAGCCTCA GCATCAACCA GTGCATCAGC	4320
TTCAGCCTCA ACAAGTGCTT CAGCCTCAGC GTCAGACCAG TGCCTCGGCT TCAGCAAGTA	4380
CCAGTGCGTC ACTTCAGCAA GCACAAGTGC GTCAGCTTCA GCATCAACCA GTGCTTCGGC	4440
TTCGGCATCA ACAAGTGCCT CAGCATCAGC ATCAACGAGT GCG	4483

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2550 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

1379

GTACCTCAGC	GTCCTTCCGC	CTCAACCAGT	GCGTCCGCTT	CAGCAAGCAC	AAGTGCGTCA	60
CCTCAGCAAG	TATCTCAGCG	TCTGAATCGG	CATCAACGAG	TGCGTCGGCC	TCAGCAAGCG	120
CAAGTACCTC	AGCGTCACTT	CCGCCTCAAC	CAGTGCGTCG	GCTTCAGCAA	GCACAAGTGC	180
GTCACTCAG	CAAGTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCGTC	TGAGTCAGCA	240
TCAACGAGTA	CGTCAGCCTC	AGCAAGCACA	TCAGCTTCTG	AATCGGCATC	AACCAGTGCG	300
TCAGCCTCAG	CATCGACAAG	CGCCTCAGCT	TCAGCAAGTA	CCAGTGCTTC	AGCCTCAGCG	360
TCGACAAGTG	CGTCGGCCTC	AACCAGTGCA	TCTGAATCGG	CATCAACCAG	TGCGTCAGCC	420
TCAGCAAGTA	CTAGTGATC	AGCTTCAGCA	TCAACGAGTG	CATCGGCTTC	AGCATCAACC	480
AGTGCCCTCGG	CTTCAGCGTC	AACCAGTGCG	TCAGCTTCAG	CAAGTACCAG	TGCTTCAGTC	540
TCAGCATCAA	CAAGTGCTTC	AGCCTCAGCA	TCGACAAGTG	CCTCGGCTTC	AGCAAGCACA	600
TCAGCATCTG	AATCAGCGTC	GACAAGTGCG	TCGGCCTCAA	CCAGTGATC	TGAATCGGCA	660
TCAACCAGTG	CGTCAGCCTC	AGCAAGTACT	AGTGATCAG	CTTCAGCATC	AACGAGTGCA	720
TCGGCTTCGG	CGTCAACCAG	TGCATCAGAG	TCAGCAAGTA	CCAGTGCGTC	AGCTTCGCA	780
TCAACAAGTG	CCTCGGCTTC	AGCAAGCACA	TCAGCATCTG	AATCAGCGTC	AACCAGTGCT	840
TCGGCTTCAG	CAAGTACCAG	TGCTTCAGCT	TCAGCATCAA	CCAGCGCCTC	GGCCTCAGCA	900
AGCACCTCAG	CTTCTGAATC	GGCCTCAACC	AGCGCCTCGG	CCTCAGCAAG	CACCTCAGCT	960
TCTGAATCGG	CCTCAACCAG	CGCCTCAGCC	TCAGCATCAA	CGAGTGCTTC	GGCTTCAGCA	1020
AGCACAAGCG	CCTCGGGTTC	AGCATCAACG	AGTACGTCAG	CTTCAGCGTC	AACCAGTGCT	1080
TCAGCCTCAG	CATCAACAAG	TGCGTCAGCC	TCAGCAAGTA	TCTCAGCGTC	TGAATCGGCA	1140
TCAACGAGTG	CGTCTGAGTC	AGCATCAACG	AGTACGTCAG	CCTCAGCAAG	CACAAGTGCT	1200
TCAGCCTCAG	CAAGTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCGTC	CGCTTCAGCA	1260
AGTACTAGCG	CCTCAGCATC	AGCGTCAACA	AGTGCTTCGG	CTTCAGCCTC	AACGAGTGCG	1320
TCTGAGTCAG	CATCAACGAG	TACGTCAGCC	TCAGCAAGCA	CATCAGCTTC	TGAATCTGCA	1380
TCAACCAGTG	CGTCAGCCTC	AGCATCGACA	AGCGCCTCAG	CTTCAGCAAG	TACCAGTGCG	1440
TCAGCCTCAG	CAAGTACCAG	TGCTTCAGCC	TCAGCGTCGA	CAAGTGCGTC	GGCCTCAACC	1500
AGTGATCTG	AATCGGCATC	AACCAGTGCG	TCAGCTCAGC	AAGTACTAGT	GCATCAGCTT	1560
CAGCATCAAC	GAGTGATCG	GCTTCGGCGT	CAACCAGTGC	ATCAGAGTCA	GCAAGTACCA	1620
GTGCGTCACT	TCCGCATCAA	CAAGTGCTC	GGCTTCAGCA	AGCACATCAG	CATCTGAATC	1680
AGCGTCAACC	AGTGCTTCGG	CTTCAGCAAG	TACCAGTGCT	TCAGCTTCAG	CATCAACCAG	1740

1380

CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC TGAATCGGCC TCAACCAGCG CCTCGGCCTC	1800
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGCGCC TCAGCCTCAG CATCAACGAG	1860
TGCTTCGGCT TCAGCAAGCA CAAGCGCCTC GGGTTCAGCA TCAACGAGTA CGTCAGCTTC	1920
AGCGTCAACC AGTGCTTCAG CCTCAGCATC AACAAAGTGC TCAGCCTCAG CAAGTATCTC	1980
AGCGTCTGAA TCGGCATCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC	2040
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGTGC TCAGCCTCAG CATCGACAAG	2100
CGCCTCAGCT TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC	2160
AACCAAGTGA TCTGAATCGG CATCAACCAG TGCCTCAGCC TCAGCAAGTA CTAGTGCATC	2220
GGCTTCAGCA TCAACCAGTG CCTCGGCTTC AGCGTCAACC AGTGCGTCAG CTTAGCAAG	2280
TACCAAGTGT TCAGTCTCAG CATCAACAAG TGCTTCAGCC TCAGCATCGA CAAGTGCCTC	2340
GGCTTCAGCA AGCACATCAG CATCTGAATC AGCGTCGACA AGCGCCTCAG CTTAGCAAG	2400
TACCAAGTGT TCAGCCTCAG CGTCGACAAG TCGCTCAGCT ACAGCAAGTA CTAGTGCATC	2460
AGCTTCAGCA TCAACGAGTG CATCGGCTTC GGCCTCAACC AGTGCATCAG AGTCAGCAAG	2520
TACCAAGTGT TCAGTTCAG CATCAACAAG	2550

(2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

ACCCAGCAAG TACTAGTGCA TCGGCTTCAG CAAGCACCAG TGCCTCGGCT TCAGCATCAA	60
CCAGTGCCTC AGCCTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAC	120
CTCAGCAAGT ACTAGTGCAT CAGCATCAGC ATCAACGAGT GCATCGGCTT CAGCAAGTAC	180
CAGCGCCTCA GCTTCAGCAA GCACCAAGTGC GTCAsCTCAG CAAGTACCAG CGCCTCAGCC	240
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	300
AGTGCGTCGG CTTAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	360
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG	420
AGTGCGTCCG CTTAGCAAG TACTAGCGCC TCAGCATCAG CGTCAACAAG TGCTTCGGCT	480
TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC AGCAAGCACA	540
TCAGCTTCTG AATCTGCATC AACCAGTGC TCAGCCTCAG CATCGACAAG CGCCTCAGCT	600

1381

TCAGCAAGTA CCAAGTGGTC AGCCTCAGCA AGTACCAGTG CTTAGCCTC AGCGTCGACA	660
AGTGGGTCGG CCTCAACCAG TGCATCTGAA TCGGCATCAA CCAGTGGTC AGCCTCAGCA	720
AGTACTAGCG CCTCAGCCTC AGCATCAACG AGTGGGTCGG CTTAGCAAG TACTAGTGCA	780
TCAGCTTCAG CAAGTACTAG CGCCTCAGCC TCAGCGTCGA CAAGCGCCTC AGCTTCAGCA	840
AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGGGTCGG CTTAGCAAG TACCTCAGCG	900
TCTGAATCAG CATCAACAAG TGGCTGGCT TCAGCATCAA CGAGTGCATC AGCTTCAGCA	960
TCAACAAGTG CTTAGCTTC AGCAAGTACC AGTGGGTCGG CTTAGCATC AACGAGTGCT	1020
TCAGTCTCAG CGTCAACCAG TGCCTCTGAA TCCGCATCAA CAAGTGGCTC GGCTTCAGCA	1080
AGCACCAGTG CTTGGGCTTC AGCGTCAACG AGTGGGTCG AGTCAGCATC AACGAGTGCG	1140
TCAGCCTCAG CAAGCACATC AGCTTCTGAA TCTGCATCAA CCAGTGGTC AGCTTCGCA	1200
TCAACAAGCG CCTCGGCTC AGCAAGTACA AGTGCTTCAG CTTAGCATC AACCAGTGCA	1260
TCAGCTTCAG CCTCAACAAG TGCTTCAGCC TCAGCGTCAA CCAGTGGCTC GGCTTCAGCA	1320
AGTACCAGTG CGTCAGCTTC AGCAAGCACA AGTGGGTCAG CTTAGCATC AACCAGTGCT	1380
TCGGCTTCGG CATCAACAAG TGCCTCAGCA TCAGCATCAA CGAGTGGTC AGCCGG	1436

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 735 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCAGTTGCCA CACCGTGGTC ACCAGCACCC GTTCCTGCGA TAATTTCTT TTTACCCATG	60
CGTwTGGCAA GCCAACTTG TCCTAAGGCA TTGTTAATCT TGTGGGCTCC TGTATGGTTA	120
AGGTCTTCCC GTTTGAGATA AATCTTGCTC CGCCAATATG CTGGGTCAAG TTTTTCGCT	180
AATAAAGAGG AGTTTCACGT CCTACGTACT GGCACAAAAG CTGGTTTAAT TCCTCTTGGA	240
AACTTGGGTC TGCCTGACTT TCACGGTAGG CTTCTCCAA CTCCAAAAC TGTGTCATCA	300
ATGTTTCTGG GACAAAACGT CCGCCGAATT TTCCGTAAAA TCCATCTTTA TTTGGTTCCT	360
GATATGCCAT GCTTACCCT CTCTATAAAT CTCTAATCT TTTTCATGATC TTTTGTCCA	420
TCTGTCTCCA CTCCGCTCGA TACATCTACT GCATAGGGAG TAAAGTGTG AATTGCTTTT	480
ACTACATTAT CTTCATTAAG GCCACCTGCG ATAAAGAAGG GCTGTGCTAG TCCAGTCGTA	540



1382

TCCAGTTGAC	CCCAATCAAA	GGGCTGGCCA	CTTCCTGCCA	CAGGGGCATC	AAAGAGTAGA	600
TAATCTGCCT	GAGAATTGGG	GACATGCCCA	TTTCCATCTA	CCTGCACAGC	CTGAATACTG	660
GCACAAGGCA	AATTCTCAAA	TAAATCATCT	GCCACCTGAC	CGTGAACCTG	AACCAAGTCC	720
AAGCCGGGGA	TCCTC					735

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1702 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

TACTAGCGCC	TCAGCCTCAG	CGTCAACAAG	TGCATCGGCT	TCAGCATCAA	CGAGTGCCTC	60
CGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	AGCGTCAACA	AGTGCATCGG	CTTCAGCGTC	120
AACGAGTGCG	TCTGAGTCAG	CATCAACGAG	TGCGTCAGCC	TCAGCAAGCA	CATCAGCTTC	180
TGAATCTGCA	TCAACCAAGT	CGTCAGCCTC	AGCATCGACA	AGCGCCTCAG	CTTCAGCAAG	240
TACCACTGCG	TCAGCCTCAG	CGTCGACAAG	TGCGTCGGCT	TCAGCAAGTA	CCAGTGCCTC	300
AGCCTCAGCA	AGTACCAAGT	CCTCAGCCTC	AGCGTCGACA	AGTGCCTCGG	CCTCAACCAG	360
TGCATCTGAA	TCGGCATCAA	CCAGTGCCTC	AGCCTCAGCA	AGTACTAGTG	CATCAGCTTC	420
AGCATCAACG	AGTGCATCGG	CTTCAGCATC	AACCAGTGCA	TCAGAGTCAG	CAAGTACCAG	480
TGCGTCAGCT	TCCGCATCAA	CAAGTGCCTC	GGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	540
AGCGTCAACA	AGTGCTTCAG	CTTCCGCGTC	AACCAGCGCC	TCGGCCTCAG	CAAGTATCTC	600
AGCGTCTGAA	TCGGCATCAA	CAAGTGCCTC	GGCTTCAGCA	TCAACGAGTG	CATCAGTCTC	660
AGCAAGCACC	AGTGCCTCGG	CCTCAGCAAG	CACCAGCGCG	TCTGAATCCG	CATCAACCAG	720
TGCCTCAGCT	TCAGCAAGTA	CCTCAGCATC	TGAATCAGCA	TCAACAAGTG	CATCGGCTTC	780
AGCAAGCACA	AGTGCTTCAG	CCTCAGCAAG	TATCTCAGCG	TCTGAATCCG	CATCAACGAG	840
TGCGTCCGCT	TCAGCAAGTA	CTAGCGCCTC	AGCATCAGCG	TCAACAAGTG	CTTCGGCTTC	900
AGCGTCAACG	AGTGCCTCTG	AGTCAGCATC	AACGAGTACG	TCAGCCTCAG	CAAGCACATC	960
AGCTTCTGAA	TCTGCATCAA	CCAGTGCCTC	AGCCTCAGCA	TCGACAAGCG	CCTCAGCTTC	1020
AGCAAGTACC	AGTGCCTCAG	CCTCAGCAAG	TACCAGTGCT	TCAGCCTCAG	CGTCGACAAG	1080
TGCGTCGGCC	TCAACCAAGT	CATCTGAATC	GGCATCAACC	AGTGCCTCAG	CCTCAGCAAG	1140
TACTAGCGCC	TCAGCCTCAG	CATCAACGAG	TGCGTCCGCT	TCAGCAAGTA	CTAGTGCATC	1200

1383

AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC AGCGCCTCAG CTTCAGCAAG	1260
CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC TCAGCAAGCA CCAGTGCCTC	1320
AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGCCTCGG CTTCAGCAAG	1380
TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT TCAGCATCAA CAAGTGCTTC	1440
AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG AGTGCTTCAG TCTCAGCGTC	1500
AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT TCAGCAAGCA CCAGTGCCTC	1560
GGCTTCAGCA AGTACTAGTG CATCGGCTTC AGCATCGACA AGTGCCTCTG AATCGGCATC	1620
AACGAGTGCT TCGGCTTCAG CATCAACGAG TGCCTCAGCC TCAGCAAGCA CATCAGCTTC	1680
TGAATCTGCA TCAACCAGTG CG	1702

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 941 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ACCAGTGCA CAGCTTCAGC CTCAACAAGT GCTTCAGCCT CAGCGTCAAC CAGTGCCTCG	60
GCTTCAGCAA GTACCAGTGC GTCACCTCAG CAAGCACAAG TCGCTCACTT CAGCATCAAC	120
CAGTGCCTCG GCTTCGGCAT CAACAAGTGC CTCAGCATCA GCATCAACGA GTGCGTCACC	180
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACCAGTG CATCAGCCTC AGCAAGTATC	240
TCAGCGTCTG AATCGGCATC AACGAGTGCA TCAGCATCAG CATCAACGAG TGCATCGGCT	300
TCAGCGTCAA CCAGTGCATC AGTCTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACG	360
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCCTCAGCC	420
TCAGCAAGTA CTAGTGCATC GGCTTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACC	480
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCCTCAGCC	540
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC	600
AGCGCCTCAG CTTCAGCAAG CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC	660
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	720
AGTGCCTCGG CTTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	780
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	840

1384

AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT	900
TCAGCAAGCA CCAGTGCGTC GGCTTCAGCA AGTACTAGTG C	941

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 869 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

CAGCAAGTAC TAGTGATCA GCTTCAGCAT CAACGAGTGC ATCGGCTTCT GCGTCAACCA	60
GTGCATCAGA GTCAGCAAGT ACCAGTGCGT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT	120
CAGCAAGCAC CAGTGCGTCG GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA	180
GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT	240
CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA	300
GTGCGTCTGA ATCGGCATCA ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT	360
CAGCGTCAAC AAGTGATCG GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA	420
GCGCCTCAGC CTCAGCGTCA ACAAGTGCAT CGGCTTCAGC GTCAACGAGT GCGTCTGAGT	480
CAGCATCAAC GAGTGCGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA	540
GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCGTCAGCCT	600
CAGCGTCGAC AAGTGCGTCG GCTTCAGCAA GTACCAGTGC GTCAGCCTCA GCAAGTACCA	660
GTGCGTCAGC CTCAGCGTCG ACAAGTGCGT CGGCCTCAAC CAGTGCATCT GAATCGGCAT	720
CAACCAGTGC GTCAGCCTCA GCAAGTACTA GTGCATCAGC TTCAGCATCA ACGAGTGCAT	780
CGGCTTCAGC ATCAACCAGT GCATCAGAGT CAGCAAGTAC CAGTGCCTCA GATTCCGCAT	840
GCAACAAGTG CCTCGGCTTC AGCAAGTAC	869

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAACAAGTG CCTCAGCATC AGCATCAACG AGTGCGTCAG CCTCAGCAAG TACTAGTGCA	60
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1385

TCAGCATCAG CATCAACCAG TGCATCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA	120
TCAACGAGTG CATCAGCATC AGCATCAACG AGTGCATCGG CTTCAGCGTC AACCAGTGCA	180
TCAGTCTCAG CAAGCACCAG TGCCTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA	240
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	300
TCGGCTTCAG CAAGCACCAG TGCCTCGGCT TCAGCATCAA CCAGTGCCTC AGCCTCAGCA	360
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	420
TCAGCATCAG CATCAACGAG TGCATCGGCT TCAGCAAGTA CCAGCGCCTC AGCTTCAGCA	480
AGCACCAGTG CGTCAGCCTC AGCAAGTACC AGCGCCTCAG CCTCAGCAAG CACCAGTGCC	540
TCAGCTTCAG CAAGTACCAG TGCCTCAGCC TCAGCGTCGA CAAGTGCCTC GGCTTCAGCA	600
AGTACCTCAG CGTCTGAATC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAGTGCT	660
TCAGCTTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCCTC CGCTTCAGCA	720
AGTACTAGCG CCTCAGCATC AGCGTCAACG	750

(2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 957 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

CCGGAAAACA GCTCTGGCGC TTGGTCTTGC CCAGCGTATT GCTAGTGGTG ACGTGCCTGC	60
GGAAATGGCT AAGATGCGCG TGTTAGAACT TGATTTGATG AATGTCGTTG CAGGGACACG	120
CTTCCGTGGT GACTTTGAAG AACGCATGAA TAATATCATC AAGGATATTG AAGAAGATGG	180
CCAAGTCATC CTCTTTATCG ATGAACTCCA CACCATCATG GGTTCCTGGTA GCGGGATTGA	240
TTGCACTCTG GATGCGGCCA ATATCTTGAA ACCAGCCTTG GCGCGTGGAA CTTTGAGAAC	300
GGTTGGTGCC ACTACTCAGG AAGAATATCA AAAACATATC GAAAAAGATG CGGCACTTTC	360
TCGTCGTTTC GCTAAAGTGA CGATTGAAGA ACCAAGTGTG GCAGATAGTA TGACTATTTT	420
ACAAGGTTTG AAGGCGACTT ATGAGAAACA TCACCGTGTA CAAATCACAG ATGAAGCGGT	480
TGAAACAGCG GTTAAGATGG CTCATCGTTA TTTAACCAGT CGTCACTTGC CAGACTCTGC	540
TATCGATCTC TTGGATGAGG CGGCAGCAAC AGTGCAAAT AAGGCAAAGC ATGTAAAAGC	600
AGACGATTCA GATTGAGTC CAGCTGACAA GGCCCTGATG GATGGCAAGT GGAAACAGGC	660

1386

AGCCCAGCTA ATCGCAAAAG AAGAGGAAGT ACCTGTCTAC AAAGACTTGG TGACAGAGTC	720
TGATATTTTG ACCACCTTGA GTCGCTTGTC AGGAATCCCA GTTCAAAAAC TGA CTCAAAC	780
GGATGCTAAG AAGTATTTAA ATCTTGAAGC AGAACTCCAT AAACGGGTTA TCGGTCAAGA	840
TCAAGCTGTT TCAAGCATTG GCCGTGCCAT TCGCCGCAAC CAGTCAGGGA TTCGCAGTCA	900
TAAGCCTCCG ATTGGTTCCT TTATGTTTCT AGGGCCTACA GGTGTCGGGG TATCCGA	957

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

CAAAGCGCCT CAGCTTCAGC ATCAACAAGT GCGTCGGCTT CAGCATCAAC CAGTGCCTCG	60
GCTTCAGCGT CAACCAGTGC GTCACATTCA GCAAGTACCA GTGCTTCAGT CTCAGCATCA	120
ACAAGTGCTT CAGCCTCAGC ATCGACAAGT GCCTCGGCTT CAGCAAGCAC ATCAGCATCT	180
GAATCAGCGT CAACCAGTGC TTCGGGCTTCA GCAAGTACCA GTGCTTCAGC TTCAGCATCA	240
ACCAGCGCCT CGGCCTCAGC AAGCACCTCA GCTTCTGAAT CGGCCTCAAC CAGCGCCTCG	300
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GCGCCTCAGC CTCAGCATCA	360
ACGAGTGCTT CGGCTTCAGC AAGCACAAGC GCCTCGGGTT CAGCATCAAC GAGTACGTCA	420
GCTTCAGCGT CAACCAGTGC TTCAGCCTCA GCATCAACAA GTGCGTCAGC CTCAGCAAGT	480
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTACGTCA	540
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GTGCGTCAGC CTCAGCATCG	600
ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCTTCAGCCT CAGCGTCGAC AAGTGCCTCG	660
GCCTCAACCA GTGCATCTGA ATCGGCATCA ACCAGTGCCT CAGCCTCAGC AAGTACTAGT	720
GCATCGGCTT CAGCATCAAC CAGTGCCTCG GCTTCAGCGT CAACCAGTGC GTCAGCTTCA	780
GCAAGTACCA TGTGCTTCAT GTCTCAG	807

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1068 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CATCGGCTTC AGCATCAACG AGTGCCTCCG CTTAGCAAG TACTACCGCC TCAGCCTCAG	60
CGTCAACAAG TGCATCGGCT TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTG	120
CGTCACCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTCCGT CACCTCAGCA	180
TCGACAAGCG CCTCAGCTTC AGCAAGTACC AGTGCCTCAC CTCAGCGTCG ACAAGTGCCT	240
CGGCTTCAGC AAGTACCAGT GCGTCACTC AGCAAGTACC AGTGCCTCAC CTCAGCGTCG	300
ACAAGTGCCT CGGCTCAAC CAGTGCATCT GAATCGGCAT CAACCAGTGC GTCACTCAG	360
CAAGTACTAG TGCATCAGCT TCAGCATCAA CGAGTGCATC GGCTTCAGCA TCAACCAGTG	420
CATCAGAGTC AGCAAGTACC AGTGCCTCAG CTTCGGCATC AACAAGTGCC TCGGCTTCAG	480
CAAGTACTAG CGCCTCAGCC TCAGCGTCAA CAAGTGCTTC AGCTTCGGCG TCAACCAGCG	540
CCTCGGCCTC AGCAAGTATC TCAGCGTCTG AATCGGCATC AACAAGTGCC TCGGCTTCAG	600
CATCAACGAG TGCATCAGTC TCAGCAAGCA CCAGTGCCTC GGCTTCAGCA AGCACCAGCG	660
CGTCTGAATC CGCATCAACC AGTGCCTCAG CTTAGCAAG TACCTCAGCA TCTGAATCAG	720
CATCAACAAG TGCATCGGCT TCAGCAAGCA CAAGTGCTTC AGCCTCAGCA AGTATCTCAG	780
CGTCTGAATC GGCATCAACG AGTGCCTCCG CTTAGCAAG TACTAGCGCC TCAGCATCAG	840
CGTCAACAAG TGCTTCGGCT TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA	900
CGTCAGCCTC AGCAAGCACA TCAGCTTCTG AATCTGCATC AACCAGTGCG TCAGCCTCAG	960
CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGCCTC AGCCTCAGCA AGTACCAGTG	1020
CTTCAGCCTC AGCGTCGACA AGTGCCTCGG GCTCAACCAG TGCATCTG	1068

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CAGCATCAAC GAGTGCTTCA GTTTCAGCGT CAACCAGTGC CTCTGAATCA GCTTCAACAA	60
GTGCCTCGGC TTCAGCAAGC CCCAGTGCGT CGGCTTCAGC AAGTACTAGT GCATCGGCTT	120
CAGCATCGAC AAGTGCCTCT GAATCGGCAT CAACGAGTGC TTCGGCTTCA GCATCAACGA	180
GTGCCTCAGC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCCGyTT	240

1388

CAGCGTCAAC CAGTGCCTCG GCTTCAGCGT CGACAAGTGC TTCGGCTTCA GCATCAACGA	300
GTGCGTCGGC CTCAGCAAGC GCAAGTACCT CAGCGTCAGC TTCGGCTTCA ACCAGTGCCT	360
CGGCTTCAGC AAGCACAACT GCGTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT	420
CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC ACATCAGCTT	480
CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCTTCA GCTTCAGCAA	540
GTACCAGTGC TTCAGCCTCA GCGTCGACAA GTGCGTCGGC CTCAACCAGT GCATCTGAAT	600
CGGCATCAAC CAGTGCCTCA	620

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 720 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GTATTGGGGC GCCCCAACCT CTATGTGACT ACGGATTATT TCCTAGATTA CATGgGATA	60
AACCATTTAG AAGAATTACC AGTGATTGAT GAGCTTGAGA TTCAAGCCCA AGAAAGCCAA	120
TTATTTGGTG AAAGGATAGA AGAAGATGAG AATCAATAAG TATATTGCCC ACGCAGGTGT	180
GGCCAGTAGG AGAAAAGCAG AAGAGCTGAT TAAGCAAGGC TTGGTGACGG TTAACGGCCA	240
AGTGGTGCGT GAACTAGCAA CCACTATCAA GTCAGGCGAC AAGGTCGAAG TTGAAGGTCA	300
ACCTATCTAC AACGAAGAAA AGGTCTACTA TCTGCTTAAC AAACCACGCG GTGTGATTTC	360
CAGTGTGACA GATGATAAGG GTCGCAAGAC GGTGTCGAC CTCTTGCCCA ATGTCAAAGA	420
GCGTATTTAC CCTGTGGGTC GTTTGGACTG GGATACATCA GGTGTCTTGA TTTTGACCAA	480
TGATGGGGAC TTTACAGACG AGATGATTCA CCCTCGTAAT GAGATTGACA AGGTTTATGT	540
CGCGCGTGTT AAAGGTGTGG CCAATAAGGA CAATCTCCGC CCCTTGACCC GTGGTCTTGA	600
GATTGATGGT AAGAAAACCA AGCCATAATA TATAGGTTT GTAGCCTCTA CACCATAAAT	660
ATTTGCTAAT AAAAATACTG TATTATTACC CTCTTAAGGT GCGAAATTAT TCAAGTTCTT	720

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 648 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CGCCATTTC	CATCGTACCG	CCGAAAATCC	CAGCGCCTCA	GCCATCAAAT	ATCCTATCAA	60
CGTTCTCAAA	AAAAGTGACC	GCTCTCTCAT	CATGTTTCCA	AGTGGTAGCC	GCCACTCAAA	120
CGATGTCAAG	GGGGGCGCAC	ACTskATTGC	CAAAATGGCC	AAGGTCCGTA	TCATGCCGGT	180
TACCTACACC	GGTCCCATGA	CTTTGAAGGG	CTTGATTAGC	CGTGAACGTG	TCGATATGAA	240
CTTTGGAAAT	CCAATCGATA	TCTCAGATAT	CAAGAAAATG	AATGATGAAG	GCATTGAAAC	300
AGTCGCCAAT	CGTATTCAAA	CAGAATTCCA	ACGTCTGGAC	GAAGAAACGA	AACAATGGCA	360
CAATGATAAA	AAACCAAATC	CACTCTGGTG	GTTTATCCGC	ATCCCTGCCC	TCATCCTTGC	420
TATTATCCTC	GCTATCCTAA	CCATCATCTT	TAGCTTTATC	GCAAGCTTCA	TCTGGAACCC	480
AGATAAGAAA	AGAGAAGAAC	TTGCATAGAA	GAAATGAACC	TTGGCCAAAC	AGCTAAGGTT	540
TTCATTTATA	TAGTAGATTG	GwACTAGAAT	AGTACACCTC	TACTTCTAAA	ACATTTTtag	600
AAATCGATTT	GACTGTCCTG	ATCGATTTGT	CCTAATCTTA	TTTCAATT		648

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 690 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

GTGCATCGCT	TTCAGCATCG	ACAAGTGGGT	CTGAATCGGC	ATCAACGAGT	GCTTCGGCTT	60
CAGCATCAAC	GAGTGCGTCA	GCTTCAGCAA	GCACATCAGC	TTCTGAATCT	GCATCAACCA	120
GTGCGTCCGC	TTCAGCGTCA	ACCAGTGGGT	CGGCTTCAGC	GTCGACAAGT	GCTTCGGCTT	180
CAGCATCAAC	GAGTGCGTCG	GCCTCAGCAA	GCGCAAGTAC	CTCAGCGTCA	GCTTCCGCCT	240
CAACCAAGTGC	GTCCGCTTCA	GCAAGCACAA	GTGCGTCAGC	CTCAGCAAGT	ATCTCAGCGT	300
CTGAATCGGC	ATCAACGAGT	GCGTCGGCCT	CAGCAAGCGC	AAGTACCTCA	GCGTCAGCTT	360
CCGCCTCAAC	CAGTGCGTCG	GCTTCAGCAA	GCACAAGTGC	GTCAGCCTCA	GCAAGTATCT	420
CAGCGTCTGA	ATCGGCATCA	ACGAGTGGGT	CTGAGTCAGC	ATCAACGAGT	ACGTCAGCCT	480
CAGCAAGCAC	ATCAGCTTCT	GAATCGGCAT	CAACCAAGTGC	GTCAGCCTCA	GCATCGACAA	540
GCGCCTCAGC	TTCAGCAAGT	ACCAGTGGGT	CAGCCTCAGC	GTCGACAAGT	GCGTCGGCCT	600
CAACCAAGTGC	ATCTGAATCG	GCATCAACCA	GTGCGTCAGC	CTCAGCAAGT	ACTAGTGCAT	660



CAGCTTCAGC ATCAACGAGT GCATCGGCTT 1390 690

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1003 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CGAGATTCTC TGGAGTTATG GATGTCGTTC CAATATGTGC ACGTTGGAAT GTTAGTGCTT 60  
ATATGGGGGG AACAGAATCC TCTCTTGATT GAAGACAAGC TAGTCATTAG GCTGGTTTGT 120  
CTTTTGTCA ACTGTAGTGG GTTGATATAA TAGTATTAGT GAGTGGGATA AAAGTTTCAT 180  
TTAGTTTATT CAGTACAAAT TTAACGGGTC AAGATTTATA TACTAGTGGT GTTTTGGGG 240  
CTGAGAGAAG TATCTTGATT TTATGTGTGG TTTTATACT TACAGTTGTT CTGCTCCAA 300  
GAGCTTGTAG AGAAGAATTA GCTCATAAAG GAGATTGATT ATTTTGATAT CAAAAAATG 360  
CACAGGATAA CCTGATGCAT TTTTTCGCG ACAATGCTTG CTAATTCCTT CTGTCGAATT 420  
TAGACAATTT TAAACCCCAA TTATTCACCC CAAATCTAAA AACCATCCAG AATCCTTGCC 480  
TTAGCTTAGA TCCTGGATGG TTTCTTTTTT CACCAATGG GTGTTTTTTA CTAGACAAA 540  
AAGAGTTTCC CCTTTATGGT ATAAGTGTAG AAAAAACAC AAAAGAAAG GAAACTCACA 600  
TGAACAGTTT ACCAAATCAT CACTTCCAAA ACAAGCTTTT TTACCAACTA TCTTTCGATG 660  
GAGGTCATTT AACCCAGTAT GGTGGTCTTA TCTTTTTTCA GGAAGTTTTT TCCCAGTTGA 720  
AACTAAAAGA GCGGATTTCT AAGTATTTAG TAACGAATGA CCAACGCCGC TACTGTCGTT 780  
ATTCGGATTC AGATATCCTT GTCCAGTTCC TCTTCAACT GTTAACAGGT TATGGAACGG 840  
ACTATGCTTG TAAAGAATTG TCAGCTGATG CCTACTTTCC AAAATTATTG GAAGGAGGGC 900  
AGCTTGCTTC ACAGCCAACC TTATCCCGTT TTCTTCCAG AACTGACGAG GAAACAGTCC 960  
ATAGTTTGGC ATGCCTCAAC CTTGAATTGG TCGAATTCCT TTT 1003

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 738 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

1391

CCGATGATTC TGATTGGTTT GCTCTTTACT TTGCTGGGAA TTTTGAGGTA GATCTATGAT	60
TGAAATACTA ATTGTTTTAG CTATTATCCT ATCTCTTGCT TTGATTGTAT TGGTAACTAT	120
ACAACCCCGT CAAAATCAAC TATTTTCCAT GGATGCCACT AGTAATATTG GTAAACCAAG	180
CTACTGGCAG AGCAACACCT TGGTCAAGGT GCTCACTTTA TTGGTGAGTT TGGCTTTATT	240
TATTCCTACTA TTAACCTTTA TGGTGATTAC TTATAAATAA AAGAAAACCT CAGATATTCA	300
CCTTTTGTGG ATTGGTCTGA AGTTTCTTT TTTATACTCA ATGAAAATCA AAGAGCAAAC	360
TAGGAAGCTA GCCGCackGC TCAAAACACC GTTTTGAGGT TGTAGATATA ACTGACGAGc	420
GA CTCAAAAC ACCGTTTGA GGTGTAGAT ATAAGTACG AGcGACTCAA AACACCGTTT	480
TGAGGTTGTG GATAGAACTG ACGAGcGACT CAAAACACCG TTTTGAGGTT GTGGATAGAA	540
CTGACGAAGT CgcTCAAAAC ACCGTTTGA GGTGTGGAT AGAACTGACG AAtgctCAAA	600
ACACCGTTTT GAGGTTGTGG ATAGAACTGA CGAAGCgaac ATATATACAG CAAGGCGACG	660
CTGACGTGGT TTGAAGAGTA TTACTGTCTA TATTTTGGT AAAAAATCAAC TTTTACTTGG	720
ATGAAGGTTT TTTTTTTT	738

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 695 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

CCGTCTTATC AAAGAGGTTA ACAAAGGCAC CAAATTTCTC GATACGAACG ACTTTAGCAC	60
GGTAAACTTC ATCCACTTTG GCTTCACGAA CCAAACCAGC AATAATTTCT TTGGCACGGT	120
TAATAGCATC TTGGTCACTA GAGTAGATAG ACACATTTCC TTCTTCGTCT ATATCAATCT	180
TAACACCTGT TTCAGCGATA ATCTTGTCGA TGGTTTCTCC ACCCTTACCG ATGACAATCT	240
TAATCTTGTC CACATCAATC TTGATCGTAT CAATTTTCGG AGCAGTTGGA GCCAATTCTG	300
GACGAACTTC TGGAAATGCTT GCTTCAATGA CATCAAGGAT TTCAAAACGC GCTTTCTTGG	360
CTTGAGCAAG AGCCTCCGTC AAGATTTCTG CAGTAATCCC TTGAATCTTG ATATCCATTT	420
GAAGGGCTGT AATCCCATCA CGAGTACCTG CAACCTTGAA GTCCATATCT CCAAAGTGAT	480
CTTCCAAACC TTGGATATCT GTCAATACTG TGTAGTTATT TCCATCTGAG ATAAGCCCCA	540
TAGCAATACC AGCTACTGGC GCCTTGATTG GCACACCACC AGCCATAAGG GCAAGAGTTC	600

1392

CCGCACAGAT AGAAGCTTGA GATGAAGAAC CGTTTGATTC CAAAACCTCT GCTACTAGAC	660
GGATAGCGTA GGGGAATTCT TCCAAGCTTG GCAGG	695

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 691 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACATCTTAT CTAAATACAT GCTAATATAT TTAGATACAA ACATTCCAAC TTGATAATTT	60
TCACTCATCT TTCATCATTC CTTATACAAC TATGCAGTAT AAATAGAATA GTTTTCTCAT	120
CAGAATGAGA CTATTTTAAT ATTAGATCCC CAATTATTCA CCCCAAATCT AAAAACCATC	180
CAGAATCCTT GCCTTAGCTT AGATCCTGGA TGGTTTCTTT TTTCACCCAA TGGGTGTTTT	240
TTACTAGACA AAAAAGAGTT TCCCCTTTAT GGTATAAGTG TAGAAAAAA CACAAAAAGA	300
AAGGAAACTC ACATGAACAG TTTACCAAAT CATCACTTCC AAAACAAGTC TTTTACCAA	360
CTATCTTTTCG ATGGAGGTCA TTTAACCAG TATGGTGGTC TTATCTTTT TCAGGAACTT	420
TTTTCCAGT TGAAACTAAA AGAGCGGATT TCTAAGTATT TAGTAACGAA TGACCAACGC	480
CGCTACTGTC GTTATTCGGA TTCAGATATC CTTGTCCAGT TCCTCTTTCA ACTGTTAACA	540
GTTTATGGAA CGGACTATGC TTGTAAAGAA TTCTCAGCTG ATGCCTACTT TCCAAAATTG	600
TTGGAAGGAG GGCAGCTTGc TTCACAGCCA ACCTTATCCC GwTTTCTTTC CAGAACTGAC	660
GAGGAAACAG TCCATAGTTT GCGATGCCTC A	691

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

ATCTCTCTGC GTAATGGTCC TCAGATAACT CTGATGATGT GTGGCGATAT AGAACTGAGC	60
CAAGTTATGC CTAAAGGGCC TTAGGAATAG GAGCTTTCAC AAGCTTATCC AGATGATTAT	120
CTTTTACTCG TTATGGACAA TGCTATATGG CATAAATCAA GTACCTTAAA GATTCCGACT	180
AATATTGGCT TTGCATTTAT TCCTCCATAC ACACCAGAGA TGAACCCCAT TGAACAAGTG	240

1393

TGGAAAGAGA TTCGTAAACG TGGATTTAAG AATAAAGCCT TTCGAACTTT GGAAGATGTC	300
ATACAAGGAC TGGAGAAGGA GGTGATAAAG TCCATCGTTA ATCGGAGACG GACTAGAATG	360
CTTTTGTAAA ACAGATGAGT ATAAAAAGAA AGTCCTCATT TCAATAGAAA TCACGACTTT	420
CTGATGAATT TATAGTAAAA TGAAATAAGA ACAGGATAGT CAAATCGATT TCTAACAATG	480
TTTTTAGAAGC AGAGGTGTAC TATTCTAGTT TAAATCCACT ATATTGGGG AGTGATAGAA	540
AAGCCCTTCA TCAGCCAATC TACTTGTTCG GGTGCGAGAG CTTTGACATC CTTTCTGTGA	600
CTGGACCAAG TCAGTTTTCG GTTCTCAAAG CGTTTATATA ATATCCAAAA TCCTTGACCA	660
TCCCAGTAAA GAACTTTAAA GCGGTCTTTA CGTCCACCAC AAAAGAGAAA GACTTGATCG	720
GAGAAAGGAT CCAATTCAAA GTGGGTTTGG	750

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 738 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TCAAATTCTT CGTGGTCCGC ATATCTnTCT TCGTACACGG CAGTCACTTG GTCTTTCCT	60
ACTCGAGTCG CAGCTTCACG GGCCAATTTC TCTTCTACTT GAACTGCCCTT TTGGAGGTCA	120
CTGTGTAGG CTGCAATGAT TTCAGCTTGC AATTCAGCAT CCACGTGAAG CAATTCCACT	180
TCTGCTTTTT CTTTACCGAC AGCAGCAACG ATTTCTTCTT GGAAGGCAAT CAATTCTTTG	240
ACAGCTTCGT GCCCTTTAAG GAGCGCTTCC AACATGATTT CTTCTGACAA TTCTTTGGCA	300
CCAGACTCTA CCATGTTGAT AGCGTGCTTG GTTCCAGCTA CTGTCAATTC AAGAAGAGAT	360
TGCTCTGCTT GTTCTTGACT TGGGTTGATG ATGATTGGC CATCTACATA TCCCCTTGT	420
ACCCAGCAA TTGGTCCGTC AAATGGAATA TCTGAAATAG ACAGTGCCAA AGATGAACCA	480
AACATAGCAG CCATGGGTGC AGATGCATTT TCATCATAAG AAAGCACTGT ATTGATGACT	540
TGGACTTCAT TACGGAAACC TTCCGCAAAC ATAGGACGAA TCGGACGGTC AATCAAACGC	600
GCTGTCAAGG TCGCATCTGT TGAAGGACGT CCTTCACGTT TCATAAAGCC ACCAGGAAAC	660
TTCCCAGCCG CATAATTTT TTCTTCGTAG TTGACTTGA GTGGGAAGAA ATCCTCAGTT	720
GCCATTTTCT GGGGATCC	738

(2) INFORMATION FOR SEQ ID NO: 384:

1394

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 657 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

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CCCCCTATTT ACCGTGGACT AAAGTTGTAC AAGAAAAGTG CAAATAAGAA ATCTCCAGAT      60
TAGGAACTAT ATATGAGTTC TCTAGTCTGG AGATTTTTC AATAGACTTCG TTATTGGGCG      120
GTTACTTTTCG AAACCTTGAA AACTTCAAAA AACGGATTTT TATCGCTTTC AAATTCTTTT      180
GGGGTCAAAC TCAGTAACTT ATTCGCCTTG TAGACTTCAT GACGCTCAGG GTATACTTTC      240
AAGGTCCCAA ATAGCCAAGA ATCGTCAGCG ATATTATCTG AATCATCTCC TTCTTGTTC      300
CCTTTAGTTC GCCTGAGGAC AGCCTTGACA CGCGCCAGAA TTCTCTAGGG CTAAAAGGCT      360
TGGTCAGGTA GTCATCAGCC CCTAATTCCA AGGCCAAAAC CTTATCAAAT TCATCACTTT      420
TCGCAGAAAC CATCATAATT GGAGTTTGA CGCCTTTGGC TCTCAGCCGC TTACAAACTT      480
CCATGCCATC TAATTGTGGT AACATGATAT CAAGCAAGAT AAAATCAAAG GGTTCGTGTTT      540
CTGCCAAAGC TAAGGCCTTC CGTCCATTG TCACCAATTG AGTAGAAAAG CCTTCCTTAC      600
TTAAATGGTA GTCAAGCAAT TTCAGAATGT GTTCTTCATC ATCCACTAAT AAGACTT      657

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(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 586 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

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CCGCATCAGC ATCAACGAGT GCATCGGCTT CACGTCAACC AGTGCATCAG TCTCAGCAAG      60
CACCAGTGCG TCGGCTTCAG CATCAACGAG TGCTCAGCC TCAGCAAGTA TCTCAGCGTC      120
TGAATCGGCA TCAACGAGTG CGTCAGCTCA GCAAGTACTA GTGCATCGGC TTCAGCAAGC      180
ACCAGTGCCT CGGCTTCAGC ATCAACGAGT GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT      240
GAATCGGCAT CAACGAGTGC GTCACCTCAG CAAGTACTAG TGCATCAGCA TCAGCATCAA      300
CGAGTGCATC GGCTTCAGCA AGTACCAGCG CCTCAGCTTC AGCAAGCACC AGTGCCTCAC      360
CTCAGCAAGT ACCAGCGCCT CAGCCTCAGC AAGCACCAGT GCCTCAGCTT CAGCAAGTAC      420
CAGTGCCTCA CCTCAGCATC GACAAGTGCG TCGGCTTCAG CAAGTACCTC AGCGTCTGAA      480

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1395

TCAGCATCAA CGAGTGCCTC AGCTTCAGCA TCAACCAGTG CCTCAGCCTC AGCAAGTATC 540  
 AGTTCGCTCAG CTTCAGCATC AACGAGTGCG TCAGCTGCAG CAAGTA 586

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 451 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CGTCGGCTTC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAAGTGCT TCAGCTTCAG 60  
 CAAGTACCAG TGCCTCGGCT TCAGCATCAA CGAGTGCTTC AGTCTCAGCG TCAACCAGTG 120  
 CCTCTGAATC CGCATCAACA AGTGCCTCGG CTTCAGCAAG CACCAGTGCT TCGGCTTCAG 180  
 CGTCAACGAG TGCCTCTGAG TCAGCATCAA CGAGTGCCTC ACCTCAGCAA GCACATCAGC 240  
 TTCTGAATCT GCATCAACCA GTGCGTCAGC TTCCGCATCA ACAAGCGCCT CGGCCTCAGC 300  
 AAGTACAAGT GCTTCAGCCT CAGCATCAAC CAGTGCATCA GCTTCAGCCT CAACAAGTGC 360  
 TTCAGCCTCA GCGTCAACCA GTGCCTCGGC TTCAGCAAGT ACCAGTGCCT CAGTTcAGCA 420  
 AGCACAAGTG CGTCAATTTA GCATCAACCA G 451

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 425 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCTCAGCAAG CACCATTGCG TCGGCTTCAT CAAGCACCAG CGCGTTTGAA TCCGCATCAA 60  
 CCAAGTGCCTC AGCTTCAGCC AAGTTACCTC AGCATCTGAA TCAGCATCAA CAAGTGCATC 120  
 GGCTTCAGCA AGCACAAGTG CTTCAGCtCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA 180  
 ACGAGTGCCT CCGCTTCAGC AAGTACTAGC GCCTCAGCAT CAGCGTCAAC AAGTGCTTCG 240  
 GCTTCAGCCT CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC 300  
 ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA 360  
 GCTTCAGCAA GTACCAGTGC GTCAGCCTCA GCAAGTACCA GTGCTTCAGC CTCAGCGTCG 420

ACAAG 1396 425

(2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 572 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

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AGAGGATCCC CGGATCCTCA GTCGCTGAGA TAACTCCTTT GGGCTTGTC ATCATGTAGT      60
AGACAAACTC TTCATACTCC AACACTTGCC CATTTTATGC GAATCTCATC TATTTTCTCT      120
TTTTTTTGCA ATTTAGCTGA TTTTCTTTT TTACCATTTA CAGTCACGCG CCCAGCCTTG      180
AGCAAGTTT TGACCTCAGT CCGACTTCCC ACCGCACAGG CAACTAAAAA TTTATCTAAT      240
CTCATAGAAC TATTATATCA TATCAAAAGG AGGCTAGTAC AATGACCAAC CTCCTTTTCG      300
TTTCATACTC TTCAAAAATC TCTTCAAACC GCGTCAACGT CGCCTTGCCG TATATATGTT      360
ACTGACTTCG TCAGTTCTAT CTGCAACCTC AAAACAGTGT TTTGAGCTGA CTCGTCAGT      420
TCTATCTGCA ACCTCAAAGC AGTGCTTTGA GCATCCTGCG GCTAGTTTCC kAGTktGCTC      480
TTTGATTTCW ATTGAGTATC AGATTAGGA AATTAACTTC CTCGkCTCCA AAAAAkAGCT      540
AAAACAATCA AGGCTCCTAA AATCGCTGGG AT                                         572

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(2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 505 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

```

CAACAAGTGC CTCGGCTTCA GCATGCACAA GTGCTTCAGC TTCAGCATGT ACCTGAGCGT      60
CTGAATCAGC ATCAACGTGT GCGTCCGCTT CAGCATGTAC TGCTGCCTCA GCATCAGCGT      120
CAACAwGTGC TTCGGCTTCA GCGTCAACGA GTGCGTCTGA GTCAGCATCA ACGAGTACGT      180
CAGCCTCAGC AAGCACATCA GCTTCTGAAT CTGCATCAAC CAGTGGCTCA GCCTCAGCAT      240
CGACAAGCGC CTCAGCTTCA GCAAGTACCA GTGCGTCAGC CTCAGCAAGT ACCAGTGCTT      300
CAGCCTCAGC GTCGACAACT GCGTCGGCCT CAACCAAGTGC ATCTGAATCG GCATCAACCA      360
GTGCGTCAGC CTCAGCAAGT ACTAGCGCCT CAGCCTCAGC ATCAACGAGT GCGTCCGCTT      420

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1397

CAGCAAGTAC TAGTGCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA GCAAGTACCA 480  
 GCGCCTCAGC TTCAGCAAGC ACCGG 505

(2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 447 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GCTAAGACTA CCTCATTAGG GGCATAGGCT GCTAAAATAA CTGCAGCTGT GGTTAATGAC 60  
 AATACTGTAC TTTTTCAT TTTAATTCCT TACATATTTA TATAACTTCC AATAGATAAT 120  
 AAACTTTAAC TTTGCTAGCC TTTGTTATAA AAAGTTTAC TAAGTATTAT CTAGGAAATA 180  
 GAGTAGTACA TTTATATATA ATTGTTATCT CTCTATAAAA ACAGTATATC ATTTAAAAA 240  
 ATTTAAGTCA AAAAAATTA CATTAGTTAA TTTATTTTTT AGCACACATT AAAAAATAAG 300  
 ATTAGTACTC AATGAAAATC AAAGAGCAA CTAGGAAACT AGCCGCAGAT TGCTCAAAAC 360  
 AGTGTTTTGA GGTGTAGAT GGAATGACGT AGTCAGCTCA AAACACTGTT TTGAAGTTGT 420  
 GGATAGAACT GACGAAGTCG GTACCGA 447

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 572 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

AGCACTTGTC GTTGAATTCT ACAACAAAT GTTGAATAT TTTATTGAAT AAGATAGGCC 60  
 TTGATATTAA GCACTTTGGG ACGTCTCCC TTAGTGCTTT TTTGATTCT CTTAGTATCC 120  
 AGCTATAATC GTTGAGACAT AACTAGACCG ATATAGTCCA AAGTGATATA GTAAATGAA 180  
 CCAAAAATAG TACACAATGT GGTATAATCC TTTTATGGCA TATTC AATAG ATTTTCGTAA 240  
 AAAAGTTCTC TCTTATTGTG AGCGAACAGG TAGTATAACA GAAGCATCAC ACGTTTCCCA 300  
 AATCTCACGT AATACCATT ATGGCTGGTT AAAGCTAAAA GAGAAAACAG GAGAGCTAAA 360  
 CCACCAAGTA TAGTGTATTG AATCTATAAC AGTACACCTT GGCTGCTAAA ATATTTCTAT 420



1398  
AAATTAATTT GACTTTCCTG ATAGAGATGT TCACATCTTA TTTCAAATA CTATATAAGT 480  
TCTATAATCT CTTTATAAGA TTTGCCCATC AGACAAAATA GAACGATTG AAGGCGTTTA 540  
TGATATTTAG CTGTACGAGA GTCTTTTAAA AG 572

MISSING UPON TIME OF PUBLICATION

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person approved by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PUT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by the applicant in the individual case.

**UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the International publication of the application.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapse, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever two dates occurs earlier.

**SINGAPORE**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

**NORWAY**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegians Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

**AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

**FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

**ICELAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected in the art.

**What Is Claimed Is:**

- 25           1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-391.
- 30           2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.
- 35           3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 40           4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising the following elements:
- 45           a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391;
- b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
- c) retrieval means for obtaining said homologous sequence(s) of step (b).
- 50           6. A method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
- 55

60 7. A method for identifying an expression modulating fragment of  
*Streptococcus pneumoniae* genome comprising the step of comparing a database  
comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a  
representative fragment thereof, or a nucleotide sequence at least 95% identical to  
the nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a  
nucleic acid molecule comprised of a complementary nucleotide sequence to said  
65 target sequence, wherein said target sequence comprises sequences known to  
regulate gene expression.

70 8. An isolated protein-encoding nucleic acid fragment of the *Streptococcus*  
*pneumoniae* genome, wherein said fragment consists of the nucleotide sequence of  
any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3, or a  
degenerate variant thereof.

75 9. A vector comprising any one of the fragments of the *Streptococcus*  
*pneumoniae* genome SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a  
degenerate variant thereof.

80 10. An isolated fragment of the *Streptococcus pneumoniae* genome,  
wherein said fragment modulates the expression of an operably linked open reading  
frame, wherein said fragment consists of the nucleotide sequence from about 10 to  
200 bases in length which is 5' to any one of the open reading frames depicted in  
Tables 2 and 3 or a degenerate variant thereof.

85 11. A vector comprising any one of the fragments of the *Streptococcus*  
*pneumoniae* genome of claim 8.

12. An organism which has been altered to contain any one of the  
fragments of the *Streptococcus pneumoniae* genome of claim 8.

90 13. An organism which has been altered to contain any one of the  
fragments of the *Streptococcus pneumoniae* genome of claim 10.

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *Streptococcus pneumoniae* genome depicted in SEQ ID NOS:1-391 and Tables 2 and 3 or a degenerate variant thereof.

15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS:1-391 and Tables 2 and 3, including fragments thereof;

b) identifying members of said library which contain sequences that hybridize to said target sequence; and

c) isolating the nucleic acid molecules from said members identified in step (b).

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

a) isolating mRNA, DNA, or cDNA produced from an organism;

b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Streptococcus pneumoniae* genome to prime said amplification;

c) isolating said amplified sequences produced in step (b).

17. An isolated polypeptide encoded by any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.

19. An antibody which selectively binds to any one of the polypeptides of claim 17.

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20. A method for producing a polypeptide in a host cell comprising the steps of:

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a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Tables 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and

b) isolating said protein.



Figure 1

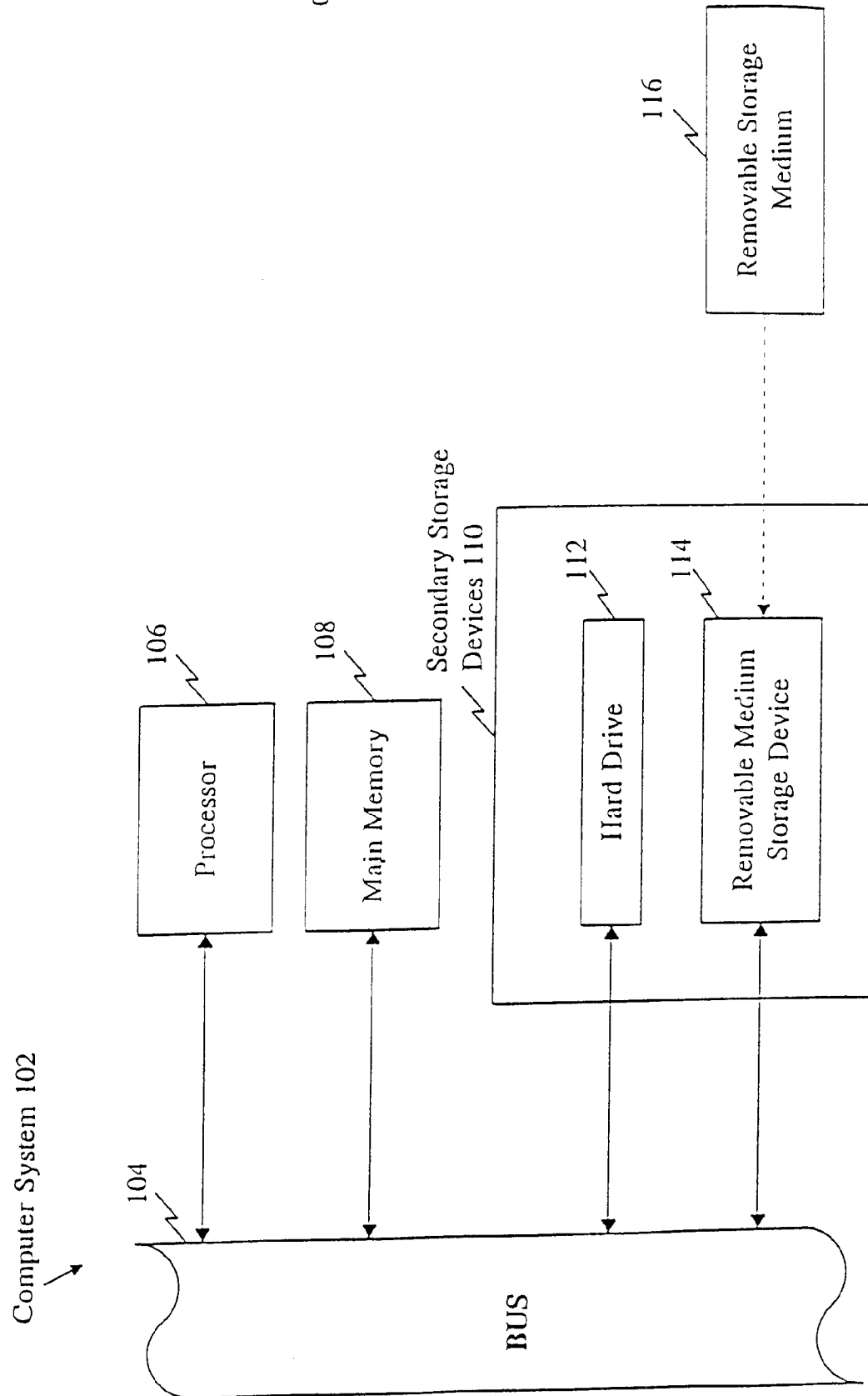


Figure 2

